AK256351 Sequence AF026197 Xanthomon M30933 E. tenella a AB045311 Xanthomon AC090645 Homo sapi AL646063 Ralstonla AC055876 Homo sapi AC05876 Homo sapi

Pseudomon Antheraea Homo sapi Rattus no

Homo sapi

Mus muscu Mus muscu

AC090533

AF051726 Mus muscu AL603702 Mouse DNA

Mus muscu

Mus muscu Caulobact

Rattus no

Homo sapi **Drosophil**

Rattus no Pseudomon

AE00457

Deinococc Caenorhab

Rattus no

AB012767 AE001876 AF067607 AC099443 AL606742 AB073377 M15101 P.0

Mus musco

Oryzias

.cynomolgi

Pseudomon

score:

Sequence: Title: Perfect

nucleic

Run on:

Scoring table:

Searched:

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Song, X., Fan, H. and Wei, Z.M.
Song, X., Fan, H. and Wei, Z.M.
Receptors for hypersensitive response elicitors and uses thereof
Patent: WO 0170988-A 8 27-SEP-2001;
Eden Bioscience Corporation (US)
L. 342
/organism="Xanthomonas campestris pv. pelargonii"
/db_xref="taxon:31612"
83 a 94 c 109 9 56 t
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Xanthomonas campestris pv. pelargonii
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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Sequence 8 from Patent W00170988.
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LMFLCHR34_11
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                                                                         June 28, 2002, 10:21:53; Search time 1822.67 Seconds (without alignments) 3926.589 Million cell updates/sec
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                                                                                                                                                       342 atggactctatcggaaacaa......gcagcctgggcggcaacgcc 342
                                                                                                                                                                                                                                                                         3595312
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                          1797656 seqs, 10463268293 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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BASE COUNT ORIGIN

Description

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sig_peptide
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Zhu,W. and White,F.F.
HprXo is a regulator of hrp gene expression in Xanthomonas oryzae
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2hu,W. and White,F.F.
Direct Submission
Submitted (22-88-1997) Plant Pathology, Kansas State University,
Throckmorton Hall, Manhattan, KS 66506, USA
4 (bases 1 to 10096)
White,F.F., Zhu,W. and Magbanua,M.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-FEB-2000) Plant Pathology, Kansas State University, 4024 Throckmorton Hall, Manhattan, KS 66506, USA Sequence update by submitter
On Mar 30, 2000 this sequence version replaced gi:4003499.
Location/Qualifiers
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                                                                                               Xanthomonas oryzae pv. oryzae
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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                                             aatcaggagtgtggcaacgaaccacagaacggtcaacaggaaggcctgagtccgttg
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/organism="Xanthomonas oryzae pv. oryzae"

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1.5e-62;
nes 0;
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Zhu,W., MaGbanua,M.M. and White,F.F.
Identification of two novel hrp-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cluster of xanthomonas oryzae pv. oryzae
J. Bacteriol. 182 (7), 1844-1853 (2000)
           Pred. No. 1.5
0; Mismatches
 Score 342;
Pred. No. 1
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          Best Local Similarity 100.
Matches 342; Conservative
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 6 /note="adjoins with sequence presented in GenBank

misc_feature

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/translation-"MIFAAALACAAPFARADCFEEAAGYQHVNFWVLRAIAWQESRGR
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GNTWAAVGAYHSETPGERDKYAHAIHSILLRLGVMVNRASDPAGWRGAAMRWHRALHQ
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NKAKIVSSPQVATLDNVEAVMDHKQQAFVRVSGYASADLINLSAGVSLRVLPSVVPGS
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PGIARNGVIYVLSSFIAYGQPADALAKIQTVGLVGVVFKEAPIGLLIGFAASTVFWIA
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DGAMLRIWGANESKSATLSLGTASTKSLRDALARWRLDDSRFPVRYDEAAHVAVYSGF
                                                                                                                                     /note="lysozyme related protein; hrp-associated protein"
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complement(4206. .5036)
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Accession Number AF23 complement(129. .908)
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ESVGLLIDDLAGYNNVQMTNPLSGQOSTPVSTVLLQLAIVSFYALGGMLMLLGALFES
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KLEFSNLSQPIRGVLALLLLALLISVFIAQFGEALGFLHFQQQLHDAANLGGKAGASH
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GHLILSREIAAKNQYPAIDVLASLSRVWSQIVPSDHSQAAGRIRRLIAKYNEVETLVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSOAOARAOTLIEEAOOOAEAILHDAROKAERSARLGYAAGLRROLDEWNESGLRHAF
AAETAAHRARERLAEIVARTCEHVILGHDPAALYARAAQALEGALDEAKALRVSVHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGEVCELRORDGTLLORAEVVGFSRDLALLAPFGELIGLSRETRVIGLGRPLAVPVGR
ALLGRVLDGLGEPSDGQGAIACDTWVPIQAQAPDPMRRLLIEHPMPTGVRIVDGLMTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MRVWLRSTPDAIGLDCDVVPREALASVLALDAAAVEVHARCEQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALDAARRAFDAAATKAGWTLQVELCGDADLAVGACVCEWDTGVFETDLRDQLRSLRRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MDNTRIDNAARCVQRWTDALAQLAESLDAARVAHWLGPVAASAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAPVYRRMRVIQAWSGWSELSPSALGVHANQLALIMPARLANVLIARALFSRGLAVR
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complement(8176..8937)
                                                                                                                                                                                                                                                                                                                                   /protein_id-"AAF61280.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF61281.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'protein_id-"AAF61282.1"
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/db_xref="G1:7350915"
                                                                                                                                                                           complement(5033. .5542)
/gene="hrpB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAF61284.1"
/db_xref="G1:7350916"
                                                                                                                      complement(5033. .5542)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5535. .6863)
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                                                                                                                                                                                                                                                                                                                                                               /db_xref-"GI:7350912
                                                                                                                                                                                                                                                                        /transl_table=11
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                            /codon_start=1
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/translation-"MTLIPPVQAIAGTSAAATQALSPVAAPNQALVNREQALMQSSSP
LPPAMQRVGSPSMMSRVVDVQNDGVRTIAEHIDAFSMQAPTMGLQEMAAQQIKLMHEL
SLVPNIKTMVMHSVEGLTYENVSVTLVPGGAESDAQLTASAPPRPSPWPWVVGCVVTL
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ОМРQQQHRRQHGQQQQCMNSQQQLQQCGQQQQQQLQQQMSEQQQQQQQQQQQQWPEQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="LRLLLKLLLLLLGQQKHWPERQQQQQPQPWLDRQQQQQHNQQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90348718
Draft entry and computer-readable sequence for [Unpublished (1990)
Synergen, INC., 1885 33rd St., Boulder, CO 80301] kindly submitted
by C.S.Ko 12-DEC-1989.
                                                                                                                                                                                                                                                                                                                                                                                    1320 AGGUCAGGGTGGCGATAATGGCGGTGGCCAGGGCGGCAATTCGCAGCAGGTGGGCAGC 1379
                                                                                                                                                                                                                                                                                                                                                                                                                                                             340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1440 CGCAGAATGGTGGTGGTGGTGGCGGGGTTCGGCGGCGGGTTCG 1499
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Identification and characterization of a target antigen of a monoclonal antibody directed against Eimeria tenella merozoites Mol. Biochem. Parasitol. 41, 53-64 (1990)
                                                                                                                                                                                                                                                                                                                  161 agagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaac 220
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 accagggcggcgcggcatgggcggtggcggttcggtcaacagcagcctgggcgaacg
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                    CLAGAAALYWWPNPQAGRWGGLQRLRELTTKGKAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="region of degenerate repeats"
240 c 249 g 77 t
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E.tenella antigen LPMC61 mRNA, partial cds.
M30933
                                                                                                                                                                                                                                                                                   83;
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Eimeria tenella
                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                Score 49.2; DB Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Eimeria tenella"
/db_xref="taxon:5802"
                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                          /protein_id="AAF61285.1"
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                                                                     .9331)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                     /gene="hrpB2"
complement(8939.
                                                                                                        /codon_start=1
/transl_table=11
                                                                                                                                           /product-"HrpB2"
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                                                                                                                                                                                                                                                14.48;
54.48;
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 99; Conserv
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TITLE
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DPRTNAILIRDRPERMOSYGTLIQQLDNRPKLLQIDATIIEIRDGAMQDLGVDWRFHS
QHTDIQTGDGRGGQLGFNGVLSGAATDGATTPVGGTLTAVLGDAGRYLMTRVSALETT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNGOMRLDVRIEDGOLGSNTVDGIPVITSSEIKTQAFVNEGOSLLIAGYAXDADETDL
NAVPGLSKIPLLGNLFKHRQKSGSRMQRLFLLTPHVVSP"
complement(3284. .4114)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGIARNGVIYVLSSFIAYGQPADALAKIQTVGLVGVVFKEAFIGLLIGFAASTVFWIA
ESVGLLIDDLAGYNNVQWTNPLSGQQSTPVSTVLLQLAIVSFYALGGMLMLLGALFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRWWPLTQLGPNMGAVAESFVIQQYDSMMAAVVKLSAPVMLVLVLVDLAIGLVARAAD
KLEPSNLSQPIRGVLALLLLALLISVFIAQFGEALGFLHFQQQLHDAANLGGKAGASH
                                                                                                                                                                                                                                                                         YVADNKDLKEVLRDLSASQSIATWISPEVTGTLSGKFETSPQKFLDDLAATYGFVWYY
                                                                                                                                                                                                                                                                                              DGAMLRIWGANESKSATLSLGTASTKSLRDALARMRLDDSRFPVRYDEAAHVAVVSGP
                                                                                                                                                                                                                                                                                                                      PGYVDTVSAIAKQVEQGARQRDATEVQVFQLHYAQAADHTTRIGGQDVQIPGMASLLR
                                                                                                                                                                                                                                                                                                                                             SIYGARGASVAPIAAFGANFGRVQPIGGGSSNTFGNAAQGQGGGASGTLGLPSAWFGG
ASPSDRMPVSPPLFGSGAAAGSPASVWPELSKGRRDESNPIDAGGGAELASDAPVIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MNDVTDALLALSSQGVSLLTLLALCGVRVFVMFIVLPATAQDSL
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SLQSARDELASVQQALSKLQAQAQVYADKAASARRARQAQRDAAEEEDAIETLVALRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"MREPAYTWSVLHQLKARRCERMQERLSDCRRALEHCDRELARCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLAETPLLETTLERELATLAFGRRYGKVVEVVGTMLKVAGVQVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGIARNGVIYVLSSFIAYGQPADALAKI
                                                                                                                                                             /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
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/transl_table=11
/evidence=not_experimental
/product="HrpB7"
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/product="HrpB6"
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/gene="hrpB8"
                                                                 complement(1384. .3201)
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complement(5931. .6632)
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QNGGGAGGGFGGGFGGDFSGDLGLGTNLSSDSASMQ"
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                                                                                                                                                                                                                 tcgccttcggctggctccgagcagcagctggatcagttgctcgccatgttcatcatgatg 150
                                                                                                                                                                                                                                                                                                                 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                    Gaps
                                                                                                                            Automotics: 1 to 19304)
Ochiai, H., Inoue, Y., Hasebe, A. and Kaku, H.
Construction and characterization of a Xanthomonas oryzae pv.
oryzae bacterial artificial chromosome library
FEMS Microbiol. Lett. 200 (1), 59-65 (2001)
                                                                                                                                                                                                                                                                                                        151 atgctgcaacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcag
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Xanthomonas oryzae pv. oryzae
                                       Length 767;
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hrp gene cluster l
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/organism="Xanthomonas oryzae pv. oryzae"
/strain="MAFF 311018"
                                                                               0; Mismatches 129; Indels
                                       DB 3;
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Xanthomonas oryzae pv. oryzae DNA,
                                     Score 48.6;
Pred. No. 1.
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Matches 126; Conserv
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CLAGAAALYWWPNPQAGRWGGLQRLRELITKGKAG"
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9113. 10192
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/gene="hrpB4"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I. (Dases I to 162869)

E. Luo,C., Bao,J., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,C., He.,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., L
                                                                                                                                                                                                               /db_xref="G1:9711589"

Translation="MSEEKTEKPTEKKLRDARKDGEVPVSPDVTAAAVLFGALLVMKS
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TLMPWIIGLAYETPLDISQIAMRTLSMLFALGVLLFILVGAADWSVQHWLFIRDKRMS
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Homo sapiens chromosome 3 clone RP11-556G18 map 3p, complete
sequence.
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Luo,C., Bao,J., Bao,Q., Bian,X., Cao,T., Chen,C., Chen,J.,
Ding, H., Dong,W., Fan,H., Feng,X., Gong,J., Guan,Q., Gu,X., Guo,D.
Guo,Z., Hel.., Huang,F., Jin,Y., Rang,N., Li,C.,
Li,F., Li,G., Li,J., Li,L., Li,S., Li,T., Liu,Y., Liu,N., Liu,B.,
Liu,Y., Li,W., Li,Y., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L.
Song,S., Sun,M., Sun,W., Sun,Y., Tan,X., Tao,R., Wang,H., Wang,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, J., Wang, J., Wang, L., Wang, R., Wang, X., Wang, X., Wang, Y., Wang, X., Wang, X., Wang, Y., Wang, X., Wang, X., Wang, Y., Wang, X., Wang, Y., Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, G., Zhang, H., Zhang, H., Zhang, L., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, X., Zhang, Y., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 agagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaac 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB ]
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                 /evidence-not_experimental
                                                                                                                                                                      /protein_id="BAB07858.1"
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/transl_table=11
                                                                                                          /product-"Hrcu"
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Center code:Beijing
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Matches 96; Conserv
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AC090645.1
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KEYWORDS
SOURCE
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Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plances-Microorganismes INRA-CNRS, DBP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jan Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGY, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire Christian.Boucherétoulouse.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABGDCMTYSVGFRSPSYRELAGHFLGFLSQTLEDNPDFEGRYTDPEQKPVERPGELPT
AMVRALAQKLNALRWTPELVGEFFGAYLTEPKDHVEFVTQPRLSLARFTARARKEGIV
LDARTQALYDAQRFWINGDTFEPSDTLLAWLSALSDQRGASAEAVDAAADLPDLMDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MNELPLYAAARGVQPGLAAGRPAQLLGGLSPRDFMRTHWQKKPL
LIRQALSPEDMRALHFPLSPDALIKLARREDVESRLIAQTRGRWTFNHGPFNERPLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKARNWTLLVQGVNLVEPAVDALMQRFRFIPDARLDDVMISFATDGGGVGPHFDSYDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ?LLQAHGRRRWRISSQNDLTLVPDLPLKILANFTPEEEFILEPGDMLYLPPHYAHDGV
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EDAIIYTYTDVAEDKYVLDGNHPLAGMALRFDLRYTDYREATAEEIEHGHYHGENGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="miscellaneous; hypothetical/global homology"
/note="Product confidence : hypothetical
Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/product="PROBABLE FKBP-TYPE PEPTIDYL-PROLYL CIS-TRANS
                                                                                                                                                                                                                                                                                                                                                                                         http://sequence.toulouse.inra.fr/R.solanacearum.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/product="CONSERVED HYPOTHETICAL PROTEIN"
/protein_id="CAN14850.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'function="cell processes; chaperoning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Product confidence : probable
Gene name confidence : probable
predicted by Codon_usage
predicted by Homology
predicted by Framen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Ralstonia solanacearum"
/strain="GMI1000"
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/protein_id="CAD14851.1"
/db_xref="G1:17428163"
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1573. .2097
'qene-"slyD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(332. .1561)
/gene="RSc1148"
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/gene="RSc1148"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"taxon:305"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="RS04604"
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                                                                                       Direct Submission
                                                            Boucher, C.A.
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     JOURNAL
REFERENCE
AUTHORS
                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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(bases 1 to 207050)

(bases 1 to 207050)

Arlat,M., Genlin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Arlat,M., Biliault,A., Brottier,P., Camus,J.C., Cattolico,L., Chandler,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T., Siguier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M., Weissenbach,J. and Boucher,C.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27493 CCAGCAGCCCCAGTAGCAGCTCCAGCAGCAGCAGCAGCAGCCCCAGTAGCAGCTCCAGCA 27552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 aaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgtt 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 ggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgc 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 gacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg-gcggcggccggca 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL646063 207050 bp DNA linear BCT 07-DE
Ralstonia solanacearum GMI1000 chromosome, complete sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ralstonia solanacearum
Bacteria, Proteobacteria, beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45; DB 9; Length 162869;
Pred. No. 5.8;
0; Mismatches 140; Indels 1
                                                                                                                                                                                                                                                                                                                                                       Insert size: 162869; sum-of-cont.gs
Quality coverage: 10.92x in Q20 bases; sum-of-cont.gs
                                                                                                                                         Sequencing vector: pUCL8: 100% of reads Chemistry: Dye-terminator: ET $5. of reads Chemistry: Dye-terminator: ET $5. of reads Chemistry: Dye-terminator Big Dye: 45% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 164941 bases at least Q40 Consensus quality: 165761 bases at least Q30 Consensus quality: 165061 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27553 GCCCCAGTAGCAGCTCTAGCAGCAGCAGCTCCAGCAGCAGC 27593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 tgggcggtggcggttcggtcaacagcagcctgggcggcaac 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-556G18"
35618 c 35228 g 46181
                                                                            --- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .162869
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                               Center project name:1% project
Center clone name: RP11-556G18
Website:http://hgc.igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                          http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
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AL646063 AL646052
AL646063.1 GI:17428161
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AL646063
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FMLHVIAPLVADFRAQYPQIELELMTSDRIIDLLEEDTDVAIRIGALRDSTLRARRLG
TRRLRVLASPAYLKAHGRPRTVDALRHHALLGFVQPESLNHWPLRGPHGDRLRITPTL
KASSGETLRQLALQGAGIVCLADFWTARDRRAGDLVQVLPEATVEIQQPIHAVYYRNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAVAGLGVIAFVGSLVFVPRDIAHAPPASLARQLQVLAQPRLLMVYAKTAIGYGGSFI
PFTFLAPILQDVAGFSAGAVGWYMLYYGVSVAAGNLWGGRLADRKGPIAALQVIFALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="G1:17428167"
/translation="MPIALLALTLSAFAIGTTEFVIVGLIPTVAADLGITLPSAGWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLYALGVAVGAPVLTALTGRLPRKALLLALMALFTLGNLLAWRAPGYAPLVLARVMTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAHGVFFSIGSTLATSLVPREKAASAIAIMFTCLTVALVTGVPLGTFIGQHFGWRETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAVLFAFTFTARYPWTAVATVLLWGAVAFGNVPGLQAYVVKQAERFAPQAVDVASGLN
IAAFNLGIAGAANAGGWIVTHLGLMHTPWIGALVVLVSLGLTAWSGALDRRGGIGPRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 cacgaggactccagccagcagtcgccttcggctggctccgagcagcagctggatcagttg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="PUTATIVE TRANSMEMBRANE EFFLUX TRANSMEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 ctgatgcagatcgtgatgcagctgatgcagaaccagggcggcggcggcatgggcggtggc 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53118 TGGGAAGCCGCCCGCCTGATGCGCGACGAGGACACCGCCGCCTATCTGCAGGTGCGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 ctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgcaaatcaggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 tgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgttgacgcagatg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 207050;
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                                                                                                                                                                                                                                     processes; transport of
confidence : putative
                                                                                                                                                                                                                                                           /note="Product confidence : putativ
Gene name confidence : hypothetical
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0; Mismatches 177;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43.8; F
                                                                                                                                                                                                                                                                                                               predicted by Codon usage predicted by Homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_1d="CAD14855.1"
                                                                       OLASRITCFLDVLEARLAQGE"
6966. .8168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="RSc1154"
/EC_number="1.-.-."
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                                                                                                                                                                                                                                                                                                                                                                     predicted by FrameD
                                                                                                       6966. .8168
/gene="RSc1153"
/note="RS04598"
                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                        /function="cell
                                                                                                                                                                                                          /gene="RSc1153"
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/gene="RSc1154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"RS04597"
                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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AC055876.5 GI:17386491
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                                                                                                                                                                                    . .8168
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Matches 150;
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                                                                                                                                                                                                                                                                                                            /translation-"MARPGAAFRAWRGIAAALAMLAATAAPAAPKGHATAAPAAPACF
                                                                                                                                                                                                                                                                                                                                     TFAVVGNVPQRPEDVAPARALLDAIDTEHPAFVVHLGNLKGRDESCTDNLLEERHDLL
                                                                                                                                                                                                                                                                                                                                                             DSTITPLIYIPGDHDWSDCGRPTAGRFDPIERLLRLRDLFYPDDNALGQRTWTVMRQS
                                                                                                                                                                                                                                                                                                                                                                                      DOAKFRSYRENARWETGGVLFVTLNVPGDNNNYKTAGGRNGEYEDRLEANROWLARAF
                                                                                                                                                                                                                                                                                                                                                                                                                 AIARQRKLPGMVIMMQADPLFEDGWERRRAPNLLDGLLRRRPHDGYLALKRQLRALAR
                                                                                                                                                                                                                                                                                                                                                                                                                                          EYDGAVLLIHGASQSFLLDRPLKDESGRPDPHVMRARTFGSPŢLDQWLEVSVTPGTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAEHSAPALEIDPRYGPFDKHTPWMQQYLKLKSAHPHTLVFYRM
GDFYELFFEDAEKAARLLDITLTSRGTTNGQPIRMAGVPFHAVEQYLAKLVKLGESVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVEAGARRLREQLGVASLVAFGCETLTAALAAAGALLNYAAATQGQSLRHVIGLTVEH
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PQARQQAIEVLLAGDWQSLRGTLRTLSDVERITGRLALLSARPRDLSSLRDTLARLPE
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PVIRAARKRLAWLEQHSADTGATPQLDLFALPSDPSDDDAAEAAAPAAPSALAEALDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trans.lation-"MKTTLEELLAFRTVVDTGSVTAAAEQLGQTVSGVSRALRRLEEK
LETTLLSRTTRRLALTDEGTAFLAHARGILAAVDEAEELIALRRQQPAGRLRVNAAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthesis, modification; dna - replication, repair,
restr./modif."
/note="Product confidence : probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="miscellaneous; not classified.regulator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="macromolecule metabolism; macromolecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="PROBABLE DNA MISMATCH REPAIR PROTEIN"
/protein_id="CAD14853.1"
                                                                                                                                                                                                    /evidence=not_experimental
/product="PROBABLE TRANSMEMBRANE PROTEIN"
/protein_id="CaD14852.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Product confidence : probable
Gene name confidence : hypothetical
                                              /note="Product confidence : probabl
Gene name confidence : hypothetical
                /function="miscellaneous; unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene name confidence: probable predicted by Codon usage predicted by Homology predicted by FrameD*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDPDSMTPRDALDALYRLKALSDASA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
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                                                                                                  predicted by Codon_usage
predicted by FrameD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="RSc1151; RS04600"
complement(3216. .5864)
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predicted by Homology
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/db_xref="G1:17428166"
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                                                                                                                                                                              /transl_table=11
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/transl_table=
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                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 6, 2001 this sequence version replaced gi:15741540.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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16127 16226: gap of 100 bp
16227 190770: contry of 174544 bp in length.
Location/Qualifiers
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/clone_lib="RPCI-11 Human Male BAC"
38922 c 39919 g 57756 t 329 others
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2677 2776: gap of 100 bp
2777 16126: contig of 13350 bp in length
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-578F21
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/chromosome="15"
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AC084023 178984 bp DNA 11near HTG 05-FEB-2002 Oryza sativa chromosome 10 clone OSJNBa0062C05, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces.
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1 (bases 1 to 178984)

Buell, R., Hsiao, J., Zismann, V., Moffat, K.M., Hill, J., Gansberger, K., Burgess, S., Jarrahi, B., Shvartsbeyn, M., Brenner, M., Feldblyum, T., Khalak, H.G., Yuan, C., Ouackenbush, J., White, O., Salzberg, S. and Fraser, C., Quackenbush, J., White, O.,
                                                                                                           Db 183403 GAAGCAGGAGGAGCAGATGCGGAAGCAGGAGGAGCAGATGCGGAAGCAGGAGGAGCAGAT 183344
                                                                                                                                                                                                Submitted (10-OCT-2000) The Institute for Genomic Research, 9712
                                                                                                                                                              171 cagcgatgcaaatcaggagtgtggcaacgaaccaccgcagaacggtcaacaggaaggcet 230
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On Feb 5, 2002 this sequence version replaced gi:18464087.
* NOTE: This is a "working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs.
* are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
* This sequence will be replaced.
* by the finished sequence as soon as it is available and the accession number will be preserved.

* 17994: contig of 17994 bp in length
                                                                  gcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccaggg 170
                                 Gaps
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gap of unknown length
contig of 85415 bp in length.
                         83;
Pred. No. 14;
); Mismatches
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51720 a 37144 c 39186 g 50461 t
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/db_xref="taxon:4530"
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Homo saplens chromosome 5 clone RP11-404K5, *** SEQUENCING IN
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* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces:

* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                            Db 124635 GCGGAGGAGGAGGGGGACAGGGGCAGATGCACCGTGGGGAGGAGAAGCACAAGCCG 124694
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                                                           gcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggectgagtccg 237
                                                                                                                                       Quality coverage: 1 in Q20 bases; sum-of-contigs
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Catarrhini; Hominidae; Homo
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                          Indels
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                        75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center Project Name: 561746
Center clone name: RP11-404K5
      ed. No. 15;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 PROGRESS ***, 4 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                      AC091951.2 GI:15320917
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN
      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 159971)
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DOE Joint Genome Institute.
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    54.0%;
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Best Local Similarity 54.0
Matches 88; Conservative
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AUTHORS
                                                                                                                                                                                                                                                                                                                   RESULT
AC091951
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stover, C.K., Pham, X.-Q.T., Erwin, A.L., Mizoguchi, S.D., Warrener, P., Hickey, M.J., Brinkman, F.S.L., Hufnagle, W.O., Kowalik, D.J., Lagrou, M., Garber, R.L., Goltry, L., Tolentino, E., Westbrook-Wadman, S., Yuan, Y., Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.M., Smith, K.A., Spencer, D.H., Wong, G.K.-S., Wu, Z., Paulsen, I.T., Reizer, J., Saier, M.H., Hancock, R.E.W., Lory, S. and Olson, W.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92982 CGGGGGAGCAGGAGGAGCAGATGCGGAAGCAGGAGGAGCAGATGCTGAAGCAGAAGAAGC 93041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93042 AGATGGGGAAGCAGGAGGAGCAGATGGGGGAGCAGGAGGAGCAGATGCGGAAGCAGGAGG 93101
                                                                                                                                                                                                                                                                                                                                                                                      107 ccgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagcc 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE004466 13409 bp DNA linear BCT 30-AUG-
Pseudomonas aeruginosa PA01, section 27 of 529 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 agggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 gcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg
                                                                                                                                                                                                                                                                    Length 159971;
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/strain="PAO1"
                                                                                                                                                                                                                                                                                                                               86;
                                                                                                                                                                                                                                                                    DB 2;
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/codon_start=1
/rransl_table=11
/product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                 Score 42.4; I
Pred. No. 21;
                                                                                                                    /clone="RP11-404K5"
a 32108 c 33093 g 47871
                           /db_xref="taxon:9606"
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Nature 406 (6799), 959-964 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .159971
/organism="Homo
                                                                                            /chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE004466.1 GI:9946120
                                                                                                                                                                                                                                                                    12.4%;
52.2%;
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                                                                                                                                                                                                                                                                                                                            94; Conservative
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LAKKEQGGENFEIVVPSISILAEPPVAVVDKVVEKKGTRKVAEATLQYLYSEEGGRIA
AQNFYRPRNQKVAAEFATQFPKLNLVTVDSDFGGWKTAQPKFFNDGGIFDQIYQAQ"
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AKRLFFFAATGLLLYLYLVRQFRRKAQAYDELHGSEQRLNRALEAVRDGLWDWDLVTD
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LRHKDGDYRWIHSRGRVLRDALGKPLHYTGVARDITLQRLKEDHLRQAAAVFDSTREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALDNWYLKRACROMREWOORGYELFVAVNVSSRLFNRGGLEERIANALEESGLEPRY
LELEVTESAVMEDFEGSLNLLCRLRILGVNLAIDDFGTGYSSLMRLKRLPVHKLKIDO
GFVAGLPGAVDDAAIARAIVALAQSMGLRVVAEGIEHQDQALFLREHGCDFGGGYWYG
                                                                                                                                                                                                                     DWQARLPDNSTPYTSTIVFLVRKGNPKG1KDWGDLTKEGVEV1TPNPKTSGGARWNFL
                                                                                                                                                                                                                                                       AAWAWAKKQYGSDEKAKDYVQALYKHVPVLDTGARGSTITFVNNQIGDVLLAWENEAF
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ERKEKFRLQQPAVKQA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLVTDAQAVIVHVNPSFERITGYRSEDVLGKTPAILKSGRQDQAFYQRLMLALREQDV
WSGEIWNRRKSGEIYPQWLHIRAVRNDQGQLTHYVGVFSDLSSIKRSENELDFLAHHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKRLQHQLDERCLLSRLGGDEFAILVENDDPEAVARLSQRILDGFNAPFDIHCQPIYI
SASLGVSLYPEDASDVDHLMQHADAALFQAKDSGRNAYAFYTRVLTARARAHVQVESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLTGLPNRVLLRERIEQALENGKDRTVAGALLLIDLDHFKHINDSLGHTTGDMLLKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRHALEHDELRVHYQPVHDLASGRIVGVESLVRWQHPERGLVPPGEFVPVAEECGLIA
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HPALQHFFRFWLWLTTGMNTREWTAIHRKHHAKCETVEDPHSPVHKGLFTVLRAGAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YKAEAKNQDTLRIYGKNCPDDWIERNLYSRFPIGGVVIMALIDLALFGALGLTVWAVQ
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SYKKWEEDLOMAWIKLESFLRLARVARVARVATPIAHRVBGKHSLDMYTAMALINNROJIM
OYRKLVIAELVKQEVKADESCYHEFRRAKLLSREYSLLQDRHHVRIDSMLAHSQAL
KVIYEKRLALQOIWAKTSANGHDMLAAIKDWVHEABASGIQSLKEFAAQLKTYSERRA
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                                                                       /product="sulfate-binding protein precursor"
/protein_id="AAG03672.1"
/db_xref="GI:9946126"
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/protein_id="AAG03676.1"
/db_xref="G1:9946130"
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/db_xref="GI:9946128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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9911. .1125
                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="PA0284"
                                                                                                                                                                                                                                                                                                                                                                         /gene-"PA0284"
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/gene="PA0286"
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/gene="PA0286"
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/gene="PA0287"
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                                                                                                                                                                                                                                                                                                                                          gene
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Abaxete-"ci:9946121"
//translation-"RSVDLMALTFLLAGFVKGVVGLGLPTVSVGLLGLAMPP
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MOAAALLIVVXALLGLAAIPUHLPARHEPWAGDLAGGATGALTAVTGVFVIPAVPYLG
ALGLORELVAALGLAAIPUHLPARHEPWAGDLAGGATGALTAVTGVFVIPAVPYLG
ALGLORELVAALGGATGALTAVTLGHGALLAGGATGALTAVTGVFVIPAVPYLG
MLRORISATLFRRCFFVGLLLLGADLAWRGFH*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-MOFNPGFSSLAALLADPGRAQMIWALMDGSARPASELALLAGVS
SASAGHLGRUVBGGVILSLEARGRNRFYRLAGPEVGQAVEALASASLLADPQRRSLPP
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DLAEVRRRRRQFACACPDWSERKPHLGGALGAALLEACLROGWIRPDDGSRALOYVSK
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DEPFGALDAKVRKELRRWLARLHEEINLTSVFVTHDQEBAMEVADRIVVMNKGVIEQI
GSPGEVYENPASDFVYHFLGDSNRLQLGNDQHLLFRPHEVSLSRSAVAEHRAAEVRDI
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SILVTLIDLPFSVSPVIAGLIYVLLFGAQGYFGEWLSDHDIQIVFAVPGIYLATLFVT
VPFVARELIPLMQEQGTQEEEAARLLGANGWGWFWHVTLPNIKWGLIYGVVLCTARAM
GEFGAVSVVSGHIRGVTNTLPLHVEILYNEYNHVAAFSVASLLLMALVILLLKQWSE
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VLADI PKEVEBAAACLGARPLQVFRHILVPALLPAWLTGFALAFARGVGEYGSVIFIA
GNMPMKTEILPLLIMVKLDQYDYTGATAIGVLMLVVSFILLLLINLLQRRIETP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRI IAGLETPDAGNIVFHGEDVSQHDVRDRNVGFVFQHYALFRHMTVFDNVAFGLRMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSSASISAATASASRRGNAGGRLALIVLAWLVFALFLLLPLYVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MSIEIRNVSKNFNAFKALDDINLDIOSGELVALLGPSGCGKTTL
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/product="probable_transcriptional regulator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="sulfate transport protein CysA"
/protein_id="AAG03669.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="sulfate transport protein Cysw"
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/db_xref="GI:9946125"
                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAG03668.1"
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/db_xref="G1:9946124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1674. .2663)
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/gene="cysA"
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/note="PA0282"
complement(3547. .4365)
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/gene="sbp"
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/transl_table=11
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963. .1661
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/note="PA0280"
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/note="PA0281"
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DIYARFLRPGTTSDIRLSRCITLLMGVAMLVLACIVNDVIAALSIAYNLLVGGLLVPI
IVYSVIGGMWSLTLTDIIQFVIKTVGIFLVLLPLSIDGAGGLARMQEVLPAGFFDLGH
                                                                                   VGALLWRRASPQGAIASIVAGCLAVIACMARDGLLANSPIVYGLLASLATFVAVSLAT
RPAASLRAQPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee,J.-S., Hwang,J.-S., Kang,S.-W., Suh,D.-S., Jin,B.-R.,
Kim,Y.-S., Lee,K.-S., Goo,T.-W., Yun,E.-Y. and Kim,K.Y..
Complete nucleotide sequence of fibroin gene cloned from Antheraea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (01-DEC-2000) Department of Sericulture and Entomology,
National Institute Agriculture Science and Technology, RDA 61
Seodun-dong, Kwonseon-gu, Suwon 441-100, Korea
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                3386 CAGGGTITCGGCACCTTCTTCGAGGCGATCCTCGAACCGGACGCGCTGGCCGCTGAAG 3327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3326 CTGACCCTGATCGCGGTGGCCATCTCGGTGCCGCTCAACCTGCTGTTCGGCGTCGGCGC 3267
                                                                                                                                                                                                                                                                                                       cagtigotogocaigitcaicaigaigaigaigcigcaacagagccagggcagcgaigcaaai 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcggcggcggcatgggc 303
                                                                                                                                                                                                                                                           0; Mismatches 108; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Ditrysia; Bombycoidea; Saturniidae; Saturniini;
                                                                                                                                                                                                                                                                                                                                                                                               caggagtgtggcaacgaaccacgcagaacggtcaacaggaaggcctgagtccgttgacg
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Kim,Y.-S., Lee,K.-S., Goo,T.-W., Yun,E.-Y. and Kim,K.Y.
Direct Submission
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                                                                                                                                                                                                                    tch 12.3%; Score 42.2; DB 1; al Similarity 49.8%; Pred. No. 27; 107; Conservative 0; Mismatches 108;
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/product="fibroin"
join(1672, .1713,1864. .9789)
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    1. .640
    /organism="Antheraea yamamai"
/db_xref="taxon:7121"
    /db_xref="taxon:711ke ele

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/db_xref="taxon:7121"
                                                                                                                            11352. .12308
/gene="speB1"
/note="PA0288"
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/translation="mrvtafvilccaloxatannihhhdeyvdnhgolverfttrhy
Ernaatrphisgnerlyftivleedpyghediyeedvvinrvpgasssaaaassasag
                                                                                                                                                                   YGSDSAAAAAAAAAAAAAGSGAGRAGGDYGWGDGGYGSDSAAAAAAAAAAAGGGG
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Pred. No. 31;
0; Mismatches 125; Indels
/protein_id="AAK83145.1"
/db_xref="GI:15077406"
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12:3%;
Best Local Similarity 50.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Clangelo, M., Collins, S., Collymore, A., Coastle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Darallano, K., Dewark, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Headrod, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P., Stange-Thomann, N., Stojanovic, N., Subramanlan, A., Talamas, J., Tesfaye, S., Titrell, A., Vasiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zlumer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 11, 2002 this sequence version replaced gi:14209777.

All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                              bp DNA linear HTG 11-FEB-2
*** SEQUENCING IN PROGRESS ***, 5
2749 GCCGCAGCTGCAGCAGCAGCAGCACCTTCAGGTGCTGGAGGATCAGGCGGCTTACGGA 2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Whitehead Institute/ MIT Center for Genome/Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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103898 126333; contig of 22436 bp in length
126334 126433; gap of 100 bp
126434 142277: contig of 15844 bp in length.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome, clone RP11-25C1
                                                                                                                                                                                                                                                                                  Homo sapiens clone RP11-25C1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                             DEFINITION
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JOURNAL
AUTHORS
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TITLE
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JOURNAL
                                                                                                                                                                                                    RESULT 13
AC016204
LOCUS
                                                                                                                                                                                                                                                                                                                                  ACCESSION
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KEYWORDS
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COMMENT

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l (bases 1 to 1722/9)

Muzny, D.M. Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Blabrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Brase, S. Brieva, M., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burchl, K.L., Byrd, N.C., Carroon, T.F., Carton, T.F., Carton, T.F., Carton, S.R., Chacko, J., Chavez, D., Chen, G., Chen, G., Chen, C., Coyle, M.D., Dathorne, S.R., David, R.R., Delgado, O., Davy, Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy, Carroll, L., Ding, Y., Dinh, H.H., Douthwalte, K.R., Delgado, O., Davy, Carroll, L., Ding, Y., Dinh, H.H., Douthwalte, K.R., Delgado, O., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Cabls, A., Garcher, T., Garza, N., Glil, R., Gorrell, J.H., Gao, J., Garcia, A., Garner, T., Garza, N., Glil, R., Gorrell, J.H., Gao, J., Garcia, A., Garner, T., Garza, N., Glil, R., Gorrell, J.H., Gao, J., Garcia, A., Garner, T., Jackson, E., Jacobson, B., Jak, Y., Johnson, R., Johlsow, S., Hume, J., Johnson, R., Lewis, L., Li, J., Liu, J., Martin, R., Martindale, M., Lucier, R., Luna, R., Martin, R., Martindale, M., Lucier, R., Luna, R., Martin, R., Martin, R., Martindale, M., Lucier, R., Luna, R., Martin, R., Martin, R., Martindale, M., Lucier, R., Luna, R., Martin, R., Martindale, R., Lucier, R., Luna, R., Martin, R., Martin, R., Martindale, R., Lucier, R., Luna, R., Martin, R., Mar
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Rattus norvegicus clone CH230-108D18, *** SEQUENCING IN PROGRESS
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L.,
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                                                                                                                                                                                 /clone_lib="RPCI-11 Human Male BAC" 32698 c 33584 g 36253 t 566 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 2;
Pred. No. 25;
                                                         /organism="Homo sapiens'
/db_xref="taxon:9606"
                                                                                                                                               /clone="RP11-25C1"
1. .142277
/organism="Homo
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Rattus norvegicus
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Best Local Similarity
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Ruiz,S., Savery,G., Schers,S., Scott,G., Shen,H., Shooshtari,N., Slason,I., Sodergren,E., Scott,G., Shen,H., Shooshtari,N., Slason,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Shooshtari,N., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,A., Tamerisa,A., Tamerisa,A., Tamerisa,A., Tamerisa,A., Tamerisa,S., Tang,H., Tansey,J., Taylor,C., Taylor,T., Tafirod,B., Thomas,N., Mall,R., Waquez,L., Vera,V., Villalon,D., Vinson,R., Mall,R., Wang,S., Wallamson,A., Walliamson,A., Walliamson,A., Walliamson,A., Walesyk,R., Woden,S., Weinstock,G. and Glbbs,R., Thou,J., Zorrilla,S., Nelson,D., Unbublish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 56 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                               Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 148335 bases at least 040
Consensus quality: 155812 bases at least 030
Consensus quality: 162105 bases at least 020
Estimated insert size: 152728; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
Quality coverage: 2.4x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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is not known and their order in this sequence record

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Jia, H., Zhang, P., Lih, S. and Roe, B.A. Mus musculus BAC Clone rp23-422n18
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Direct Submission
Submitted (28-JUN-2001) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                98 cggctggctccgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgc 157
                                                                                                                                                                                                                                                                                                                                                                  aacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtc 217
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Pred. No. 33;
0; Mismatches 156;
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NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 272545)
Li,L., Montgomery,K.T., Grills,G., Chiu,D., Decker,J., Fusina,M.,
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Pred. No. 36;
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/note="assembly_name:Contig108"
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                                                       2 (bases 1 to 272545)
Li L., Montgomery, K.T., Grills, G., Chiu, D., Decker, J., Fusina, M.,
Coltz, J., Haider, A., Hall, L., Han, J., Ioshikhes, I.P., Lee, E.,
Perera, A., Shim, C., Thomas, E. and Kucherlapati, R.
                                                                                                                            Submitted (02-MAR.2001) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave. Bronx, NY 10461, USA
On Dec 21, 2001 this sequence version replaced gi:13310871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 6.8 x in Q20 bases; sum-of-contigs estimation
Goltz,J., Haider,A., Hall,L., Han,J., Ioshikhes,I.P., Lee,E.,
Perezra,A., Shim,C., Thomas,E. and Kucherlapati,R.
High Throughput Mouse Sequencing
Onpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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g of 30444 bp in length
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Chemistry: Dye-terminator Big Dye; 1008
*Consensus quality: 257441 at least 020
*Consensus quality: 253718 at least 030
*Consensus quality: 247095 at least 040
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                                                                                                                                                                                                                                                                                 Contact: gnktm@capecod.bwh.harvard.edu
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JOURNAL
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Score 40.8; DB 2; Length 272545; Pred. No. 43; 0; Mismatches 127; Indels 0; Gaps Query Match 11.9%; Best Local Similarity 48.0%; Matches 117; Conservative

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102 tggctccgagcagcagctggtcagttgctcgccatgttcatcatgatgatgctgcaaca 161 ò

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Search completed: June 28, 2002, 11:23:05 Job time: 3672 sec

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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
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| SIDSI/gcgdata/geneseq/geneseqn-embl/NA20018.DAT:*
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                                                           Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1736436 seqs, 858457221 residues
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Xanthomonas campes	Nephila clavines	Enstein Barr Virus	Drosophila melanog	Human DNA encoding	P putida KT2440-a	DNA encoding nowel	DNA Sequence of his	Hypersensitive res	TO TO THE PROPERTY.
		AAD18127	T85356	X90924	L23322	A51260	F61055	AAS79854	C84677	AAT49316	
	QI S	2 AA	8. AA	O AA	23 AB				22 AA	8 AA	
	th DB	342 2	04 1	25 2						35 1	
	Leng	ñ	<u>5</u> 0	19	38	31;	158	433	513	103	
φ	Query re Match Length DB II	100.0	11.3	11.2	11.2	11.1	11.1	11.1	11.1	11.0	
	Score	342	38.8	38.4	38.4	38	37.8	37.8	37.8	37.6	
	Result No.	٦	7	m	4	S	9	. 7	œ	6	
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19-MAR-2001; 2001WO-US08728. 23-MAR-2000; 2000US-191649P.

		Pseudomonas solana	Hypersensitive res	DNA encoding a hyp	sol		domonas		Drosophila melanog		Drosophila melanog	Human secreted exp	Human reproductive		Nephila clavipes s	N. clavipes spider		Drosophila melanog	Human reproductive	Pseudomonas aerugi	DNA encoding anglo	Human reproductive	Protein requiating	Drosophila melanog	Human immune/haema	Human immune/haema	Human secreted pro	Human cDNA clone (Human polynucleoti	Human cDNA sequenc	Human polynucleoti	Mycobacterium tube	Human polynucleoti	Xanthomonas hrf1 p	_	E. tenella cGMP de
00077	4003	AAV39975	AAV36430	AAV83991	AAD00674	AAA14944	AAD12808	ABL23323	5117	ABL05116	ABL27665	AAA42475	AAL01496	AAQ14183	AAV23249	AAZ38195	AAQ98470	ABL27664	AAL05260	AAS51554	5239	AAL01459	AAZ57853	ABL09166	AAK72397	AAK72395	AAC02116	AAH05110	AAI61196	7588	AAI59410	AA199683	1388	4895	9159	4577
2774		-	19 AAV3	Ī	-	-	-	-	3 ABL0511		23 ABL2													-	-	22 AAK7	1 AACO	·	-	-	⋖		22 AAI81388	-	•	1 AAC6457
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11	11.	•	٠	11.0	•	11.0	11.0				٠.	10.9			10.9				10.9			10.8	10.7	10.7	10.7	10.7	10.6	10.6	0	0	10.6	。	10.6	。		10.5
37.6	27.0	•	٠.		٠		37.6	37.4	37.4	37.4	•	37.2	37.2	37.2	37.2	37.2	37.2	37.2	37.2	37	37	36.8	36.6	36.6	36.6	36.6	36.4	36.4	36.4	36.4	٠.			9	m	35.8
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ALIGNMENTS

AAD18127;

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Plant pathogen; hypersensitive response elicitor; HRE; stress resistance; disease resistance; Erwinia amylovora hypersensitive response elicitor; harpin; signal transduction; growth enhancement; insect control; virucide; fungicide; antibacterial; ss.
                                                                                                                                                                            /product= "Xanthomonas campestris hypersensitive response elicitor protein"
/note= "CDS does not include stop codon"
                                Xanthomonas campestris hypersensitive response elicitor protein cDNA
                                                                                                                                          Location/Qualifiers
            (first entry)
                                                                                                                                                     1..342
/*tag= a
                                                                                                                                                                                                                /partial
                                                                                                                  Xanthomonas campestris.
                                                                                                                                                                                                                                      WO200170988-A2
           18-DEC-2001
                                                                                                                                                                                                                                                               27-SEP-2001.
                                                                                                                                          Key
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AAT85356 standard; DNA; 2004 BP.

(EDEN-) EDEN BIOSCIENCE CORP. 01-DEC-2000; 2000US-250710P. Fan H, Wei WPI; 2001-590177/66. P-PSDB; AAE10807 Song X,

New plant pathogen hypersensitive response elicitor-receptor protein isolated from plants, which upon silencing is used to study plant signal transduction pathways leading to disease resistance and growth enhancement

Disclosure; Page 19; 78pp; English,

and insects through HRE treatment. The protein is useful for understanding the harpin (Erwinia amylovora hypersensitive response understanding the harpin (Erwinia amylovora hypersensitive response elicitor) induced signal transduction pathway in plants. The protein is useful for studying the downstream components of signal transduction pathway in plants which eventually leads to disease resistance, growth enhancement, insect control and stress resistance. Imparting disease resistance to plants through HRE treatment has the potential to treat previously untreatable diseases, treating diseases systemically which might not be treated separately due to cost and avoids the use of infectious agents or environmentally harmful materials. By HRE treatment increased quantity of seeds produced, increased percentage of seeds germinated, increased plant size, greater biomass, more and bigger fruits, etc. which results in economic benefit to cultivators. Greater yield, increased size and enhanced biomass allow greater revenue generation from the given plot of plant. The present sequence is synches, cons The present invention relates to an isolated protein which serves as a receptor in plants for plant pathogen hypersensitive response elicitors (HME). The plants are made resistant to infection by viruses, bacteria and fungi and are imparted with resistance against environmental stress

Sequence 342 BP; 83 A; 94 C; 109 G; 56 T; 0 other;

ó 121 gatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagggtgc 180 121 gatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgca 180 acgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcggcggcggcatg 300 241 acgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcggcggcggcatg 300 9 1 atggactctatcggaaacaacttttcgaatatcggcaacctgcagacgatgggcatcggg 60 0; Gaps 1 atggactctatcggaaacaacttttcgaatatcggcaacctgcagacgatgggcatcgg 181 aatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgttg 100.0%; Score 342; DB 22; Length 342; 100.0%; Pred. No. 3.8e-79; ive 0; Mismatches 0; Indels 0; 301 ggcggtggcggttcggtcaacagcatgggcggcaacgcc 342 301 99c99tggcggttcggtcaacagccagctgggcggcacgcc 342 Query Match 100.

Best Local Similarity 100.
Matches 342; Conservative 241 g g ð ò ò 셤 ò 셤 à g ð

encoding silk protesin. The production of a DNA fragment encoding silk protesin. The process involves: (a) selecting target DNA, from a silk-producing spider, that contains many repetitive and non-repetitive regions; (b) selecting a single-stranded DNA primer of at least 10 nucleotides with a sequence that is complementary to a region of the target; (c) repetitively combining the primer with melted target. DNA, incubating the mixture with nucleotides and a DNA polymerase with profereding activity to produce a DNA fragment which is complementary to the target and is at least 2 kb long. The present sequence represents a 2 kb DNA sequence which encodes the spider silk protein from Nephila clavipes. The DNA fragment can be used to make fibres, films, woven articles, e.g. for use in parachutes, sails, body armour, and absorbers (e.g. of heavy metals, biological weapons, DNA, chemicals, flavours and fragrances). The high molecular weight (90-250 kD) of spider silk proteins can be produced on a commercial scale (at over spider silk proteins can be produced on a commercial scale (at over spider silk proteins). It has better tensile strength and elasticity than commercial scale for the produced on a commercial scale (at over silkworm silk, included by the repetitive and non-repetitive regions High strength film; fibre; woven article; parachutes; sails; absorber; body armour; heavy metal; biological weapon; chemical; flavour; fragrance; Nephila clavipes; ss. 11.3%; Score 38.8; DB 18; Length 2004; 50.0%; Pred. No. 1.6; New opt. multimerised DNA sequences encoding spider silk procontg. both repetitive and non-repetitive sequences, useful making high strength films, fibres, woven articles etc. Nephila clavipes spider silk protein 2 Kb DNA sequence. Sequence 2004 BP; 481 A; 386 C; 791 G; 346 T; 0 other; Location/Qualifiers 40..1980 /*tag= a /product= Silk_protein ensures isolation of stable clones. Claim 14; Fig 1; 57pp; English. 96WO-US13767 95US-0517694 (first entry) Basel RM, Ellon GR; WPI; 1997-179272/16. (BASE/) BASEL R M. (ELIO/) ELION G R. Nephila clavipes. P-PSDB; AAW27178. WO9708315-A1. 22-AUG-1996; 22-AUG-1995; 36-MAR-1997. AAT85356; Query Match Key

813 agcagcagctggaggtgctggacaaggaggatacggtggtcttggtggacaaggtgccgg 872 110 agcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagg 169 170 gcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcc 229 Indels 97; --= Pred. No. 1.6; 0; Mismatches Best Local Similarity 50.0 Matches 97; Conservative δ g ð

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Gaps

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molecules and transcription factors. The episomes carrying desired genes can also be used to transfect cells in gene therapy, antisense therapy, for gene amplification, cell immortalisation, etc.
                                                                                                                                                                                                                                                                                                                                                     Epstein Barr Virus Nuclear Antigen 1 DNA; plasmid pCMVEBNA, EBNA 1; episome; transfection; origin of replication; EBV orip; receptor; eucaryotic host cell; recombinant cell line; ion channel; gene therapy; multiple gene expression; transporter protein; transcription factor; adhesion molecule; antisense therapy; gene amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen 1 (EBNA 1), which is obtained from commercially available plasmid pcWVEBNA. EBNA 1 protein is used to stably maintain episomes containing EBV origin of replication (orif) and a gene encoding protein or RNA of interest. Bucaryotic host cells expressing EBNA 1 protein are transfected with these episomes to produce recombinant rapid and reliable method of stably expressing multiple genes of interest. This provides a transfected cells. The episomes useful in the transfection of genes encoding receptors, transporter proteins ion channels, adhesion of genes molecules and transfection of genes.
 873 acaaggtggctatggaggacttggaagccaaggtgccggacgaggaggattaggtggaca 932
                                         289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a 5
                               230 tgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcg
                                                                933 aggtgcaggtgcagcagcagcagcagcagctggaggtgccggacaaggaggactaggtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_except= (pos:799 .800, aa:cly)
/note= "The sequence is described throughout the specification as being 1926 nucleotides long, but sequence of only 1925 bp has been given in figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method for expressing genes from recombinant eukaryotic cells,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virus Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a DNA encoding Epstein Barr
                                                                                                                                                                                                                                                                                                                    Virus Nuclear Antigen 1 (EBNA 1) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                 AAX90924 standard; DNA; 1925 BP
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                                                                                                                                   993 acaaggtgctggac 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                       cell immortalisation; ds
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                                                                                                 290 gcgccggcatgggc 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-610610/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Epstein-barr virus.
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                                                                                                                                                                                                                                                                                                                    Barr
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06-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                  675
                                                                                                                                                                                                                                                                                                                                                            102 tggctccgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaaca 161
                                                                                                                                                                                                                                                                                                                               ggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaa 281
                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 21439:
                                                                  Length 1925;
                                                                                                                                                                                                                                                                                                                                                                                            282 ccagggcggcgccggcatgggcggtggcggttcggtcaacagcagcctgggcggca
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                                                                                                 Indels
             Sequence 1925 BP; 486 A; 352 C; 872 G; 215 T; 0 other;
                                                                                Pred. No. 2;
; Mismatches 161;
                                                                  DB 20;
                                                             Score 38.4;
Pred No. 2;
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                                                               Query Match
11.2%;
Best Local Similarity 45.6%;
Matches 135; Conservative
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila;
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(ABB57737-ABB72072)

WPI; 2000-431586/37.

us-09-829-124-1.rng

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published_pct_sequences.
                                                                                                                                                             2843 TCGATGGCATCAGCGATGCTGGCGACTCTGGAGCTGGACTACTTCAGGGCGGTGTCCCTC 2784
                                                                                                                                                                                                                                                      2723 CACGATGGCCATGTCCAACTGTTCACCACCAAGGAGGAGGAGGAGGAGGAGCAGCAG 2664
                                                                                                                                                                                                        tcggctggctccgagcagcagctggatcagttgctcgccatgttcatcatgatgatgctg 156
                                                                                                                                                                                        caacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggt 216
                                                                                                                                                                                                                                         caacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatg 276
                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= PRO539
/note= "A putative Drosophila Costal-2 homologue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO539; Costal-2; homologue; kinesin-related; Hedgehog; signalin
secreted protein; transmembrane protein; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W, Goddard
Watanabe CK;
                                                                                                                  ö
                                                                                     Score 38.4; DB 23; Length 3840;
Pred. No. 2.4;
0; Mismatches 121; Indels 0;
                                                                                                                                                                                                                                                                                                        2663 CAGCAGCAGCAGCACCAGCAGATTCGGTAGCAATTGCAACGCATTGGCC 2612
                                                                                                                                                                                                                                                                                      277 cagaaccagggcggcgggcatgggcggtggcggttcggtcaacagcagcc 328
                                                  Sequence 3840 BP; 954 A; 915 C; 880 G; 1091 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fong S, Gao
A, Tumas D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human DNA encoding PRO539, a Costal-2 homologue.
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, Stewart TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
186..2678
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                           AAA51260 standard; cDNA; 3121
                                                                                       11.2%;
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99US-0119965.
99WO-US12252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0119341
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99US-0115565
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                                                                                   Query Match 11.2
Best Local Similarity 47.8
Matches 111; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200036102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2000
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Gurney AL, I
Wood WI;
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02-JUN-1999;
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12-JAN-1999
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10-FEB-1999
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                                                                                                                                                        Costal-2 is a kinesin-related protein in the Hedgehog signaling pathway. The invention concerns novel secreted and transmembrane proteins, designated PRO polypeptides. The cDNA and gene sequences are useful in the recombinant production of PRO polypeptides, as a hybridization probe to screen libraries to isolate cDNAs with sequence identity to PRO polypeptides or to map the gene encoding the PRO polypeptides and analyzing genetic disorders. The cDNA/gene can also be used to produce transgenic animals useful for the development and screening of therapeutically useful reagents. They can also be used the gene therape, e.g. to replace a defective gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1980 gaggagcagcaccagcagcagattgccttctcggaactggagtgcagctggaggagcag 2039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2040 cagaggetggtgtactggetggaggtggeectggagegegegegeetggagatggacege 2099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2100 cagetgaccetgeageagaaggageacgageagaacatgeagetgeteetgeageagagt 2159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 ggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggc 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 gagcagcagctggatcagttgctcgccatgttcatcatgatgatgcagcaacagagccag 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggc 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic plant; detection; probe; amplification; vaccine carrier; microbial production strain; biological remediation; ds.
                                                   nucleic acid molecule encodes a PRO polypeptide which is
                                                                                                                                        This cDNA encodes PRO539 a putative Drosophila Costal-2 homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 3121;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 21; Length 31
Pred. No. 2.9;
0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                          Sequence 3121 BP; 702 A; 820 C; 1114 G; 485 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2160 cgagaccacctcggtgaagggttagcagacagcaggaggcag 2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggcgccggcatgggcggtggcggttcggtcaacagcagcctg 330
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DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
MEDIZINISCHE HOCHSCHULE HANNOVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P. putida KT2440-associated DNA ORF07581,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                       Claim 1; Fig 3; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               11.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99DE-1035088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99DE-1035088
                                                                  transmembrane polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.1
Best Local Similarity 48.2
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas putida.
                  P-PSDB; AAY96730
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(GBFB )
(DKFZ-)
(MEDI-)
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31-MAR-2000; 2000US-0540217

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This invention describes novel DNA sequences (1) for specific detection of Pseudomonas putida KT2440. The invention also describes (1) recombinant expression vector containing (1); (2) prokaryotic or excombinant expression vector containing (1); (2) prokaryotic or eukaryotic cells transformed or transfected with (1) or the vector of (1); (3) production of expression products by culturing cells of (2); (2) proteins or peptides with the same sequences (A); (5) poly- or proteins or peptides with the same sequences (A); (5) poly- or proteins or peptides with the same sequences (A); (5) poly- or proteins or peptides with the same sequences (A); (5) poly- or plants that contain transformed or transfected cells of (2); (8) that the contain transformed or transfected cells of (2); (8) that that contain transformed or transfected cells of (2); (8) that that contain transformed or transfected cells of (2); (8) that that contain transformed or transfected cells of (2); (8) that that contain transformed or transfected cells of (2); (1) transgenic of detecting KT2440 using a labeled (1) or Ab as probe; and (9) DNA chips of (2); (8) that transfected the production of transgenic plants, (1), (1), and their transments, are used for detecting the presence of KT2440, particularly in presence of other.

Cor antibodies that recognize their expression products, are used for detecting the presence of KT2440, particularly in presence of other.

Cor antibodies that recognize their expression products, are used for detecting the presence of KT2440, particularly in presence of other.

Cor antibodies that recognize their expression products, are used for detecting the presence of KT2440, particularly in presence of other.

Cor antibodies that recognize their expression products, are used for detecting the National Institutes of Health, for genetic engineering work, e.g. as microbial production strains, for bological remediation and as vaccine carriers (1) are exclusive to KT2440 with no significant has a reason of the particular of the p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      survival in, and adaptation to,
                                                                                   ful as
other
                                                                                useful
                                                                 New DNA sequences specific for Pseudomonas putida KT2440, usef
Safe genetic engineering host, allow detection in presence of
related bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related pathogen P. aeruginosa). Compared with other has greater catabolic activity and better survival in
                                                                                                                                                                                                                   - - - :
- i ,
                                                                                                                                                                                                    Claim la; Page 105-106; 158pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the rhizosphere and soil.
WPI; 2001-192469/20
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129 gctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgcaaatcagga 188
                                                                                                                                                     189 gigiggcaacgaacaaccgcagaacggicaacaggaaggccigagiccgitgacgcagai 248
                                                                                                             985 GCCGGACCACTTGCTCAAGACGTTCCTGCAACGCCTTGGGCGTGCCGTTGAACAGCAGGT 926
                                           Gaps
                                                                                                                                                                                         925 GIGCITCATCGAAGAACAGCGCCAGCACCGGCITGTCGGCCATCACCGCGCTCGGGCAACT
 Score 37.8; DB 22; Length 1581;
Pred. No. 2.7;
0; Mismatches 77; Indels 0;
                                         ö
                                       .77; Indels
                                                                                                                                                                                                                                                                     865 GCTCGAACAGTTCGGCCAGCACCACAACAGGAACGTCGCG 825
                                                                                                                                                                                                                               249 gctgatgcagatcgtgatgcagctgatgcagaaccagggcg 289
ch 11.1%;
1 Similarity 52.2%;
84; Conservative
                 Best Local Similarity
Query Match
                                     Matches
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Sequence 1581 BP; 284 A; 451 C; 557 G; 289 T; 0 other;

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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                     DNA encoding novel human diagnostic protein #15658.
RESULT 7
AAS79854/c
ID AAS79854 standard; cDNA; 4335 BP.
XX
                                                                  (first entry)
                                                                                                            Human; chromosome
                                                                                                                                                                 40200175067-A2.
                                                                 13-FEB-2002
                                                                                                                                                                                      11-0CT-2001
                                           AAS79854;
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DNA sequence of human PPP2R2B

30-MAR-2001; 2001WO-US08631

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The chair and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and on the produce other types of the invention of mutations of the invention of the printed diagnostic coding sequences of the invention of the printed specification, but was obtained in electronic format directly from MIPO are the contract of the printed are the contract of the pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2575 CAGAGGCCTTCTGAGAATGACTTGGTGCCGCAGAAGCAGCAGCAGCAGGAGCAGCAGCTA 2516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                      mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 atgatgatgctgcaacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 ccgcagaacggtcaacaggaaggcctgagtcgttgacgcagatgctgatgcagatcgtg
                                                                                                                                                                                                                                                                                                                                   diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.1%; Score 37.8; DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 15658; 103pp; English.
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                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2395 CAGCAGCAGCAGCAGCAG 2375
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                                                                                                                                                                       Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 49.3
Matches 99; Conservative
                                                                                                                                                              Drmanac RT, Liu C,
                                                                                                                                                                                                                        WPI; 2001-639362/73
                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                  P-PSDB; ABG15667
                                                         23-AUG-2000;
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Microsatellite marker; human; chromosome 5q31-33; D5S402; WI-6763;
CAG trinucleotide repeat; spinocerebellar ataxia 12; SCA12; PPP2RBbeta;
brain; protein phosphatase PP2A; ds.
                                                                                                                                                                                                                                                                                       New polynucleotide for use in diagnosing spinocerebellar ataxia 12, comprises a microsatellite marker having a variable number of CAG trinucleotide repeats located on human chromosome 5q31-33
                                                                                                                                                 note= "protein _id= AAF74024.1"
                                                                                                                                                                                                                                                                                                                        Disclosure; Page 21-23; 23pp; English.
                                                                                                                                         ""PPP2R2B""
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                 Holmes SE;
                                                                                 "CAG"
                                                                                                                                                                                               16-JUN-2000; 2000WO-US40213.
                                                                2088..2366
/*tag= a
                                                                                                 /*tag= b
2473..3023
                                                                                        . 3093
                                                                                 /rpt_type=
                                                                                                                 /*tag= c
                                                                                                                                                                                                                                UYJO ) UNIV JOHNS HOPKINS
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                                                                                                                                                                                                                                                                WPI; 2001-102718/11.
P-PSDB; AAB48340.
                                                                                                                                                               WO200078943-A2
                                                                repeat_region
                                                                                                                                                                                                                                                Margolis RL,
                                         Homo sapiens
                                                                                                                                                                                                                18-JUN-1999;
                                                                                                                                                                               28-DEC-2000
                                                                                                       5'UTR
                                                                                        mRNA
                                                                                                                       CDS
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The invention relates to a microsatellite marker located on human chromosome 5q31-33 between markers D5S402 and WI-6763, comprising a variable number of CAG trinucleotide repeats. The marker is useful for CAG trinucleotide repeats in a 5'-untranslated region of an allele of PPP2RBbeta, a brain specific regulatory subunit of protein phosphatase PP2A, where if a number greater than 40 js determined, an expansion which is associated with SCAI2 is indicated. The presence of expanded trinucleotide repeats on chromosome 5q31-33 is useful for predicting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ï
                                                                                                                                                                                                                                                                                             diagnosing SCA12. Also provided are primers useful for amplifying the microsatellite marker associated with SCA12 and for diagnosing SCA12 and a probe useful for detecting expansions in a microsatellite marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2045 gaggagcetegeetttaatgeaceageegeeteeageeteetgeageageageagea 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108 cgagcagctggatcagttgctcgccatgttcatcatgatgctgcaacagagcca 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999cagcgatgcaaatcaggagtgtggcaacgaacaacgcagaacggtcaacaggaagg 227
                                                                                                                                                                                                                                                                                                                                                                                          ocated on human chromosome 5q31-33. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 1336 A; 1267 C; 1268 G; 1249 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.1%; Score 37.8; DB 22; 47.8%; Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 140; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168
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2284
271 ctgatgcagaaccagggcggcggcatgggcggtggcggttcggtcaacagcagcctg 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              772 ctggtgcagatgatgcagcagcggcgcctcggcggcggcggcaaccaggcggcggctcg 831
                                                                                                                                                                                                                                                                                                                Hypersensitive response; elicitor; Pseudomonas solanacearum; plant; disease-resistance; Escherichia coli; infiltration; virus; bacterium; fungus; pathogen; biological control agent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a hypersensitive response elicitor from Pseudomonas solanacearum. The elicitor may be used in a new method for imparting pathogen resistance to plants, by application of the elicitor in a non-infectious form to plant cells, by spraying, injection, leaf abrasion, or plant infection with recombinant bacteria (non-infectious to the host plant, e.g. Escherichia coll) expressing the elicitor as a biological control agent, to alllow recombinant protein infiltration into the plant. The method confers virus, bacterium or fungus disease-resistance on crops and
                                                        cctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 aacggicaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               712 agogaagaccagggcgcctcaccggcgtgctgcaaaagctgatgaagatcctgaacgcg
                                                                                                          gcggcggcatgggcggtggcggttcggtcaacagcagcctgggcggcaac 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - with hypersensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1035 BP; 227 A; 330 C; 368 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 37.6; DB 18; 55.3%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Imparting pathogen resistance to plants - response elicitor polypeptide or protein
                                                                                                                                                                                                                                                                                    Hypersensitive response elicitor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 51-52; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                             AAT49316 standard; DNA; 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0475775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US08819.
                                                                                                                                                                                                                                                       30-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-051614/05.
P-PSDB; AAW06600.
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ses 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wei Z;
                                                                                                                                                                                                                                                                                                                                                                                                          WO9639802-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                       19-DEC-1996
                                                                                                                                                                                                                          AAT49316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beer SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                       287
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Matches
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polypeptide or protein to control insects on plants or plants grown from seed treated with HRE. Also claimed is a method of insect control for plants that involves: (a) providing a transgenic plant or seed transformed with a DAM molecule (see AAV54606-09) encoding a HRE polypeptide or protein (see AAW75862-67); and (b) growing the transgenic plants or transgenic plants produced from the transgenic seeds to control insects. HRE prevents direct insect damage to plants by feeding injury. It kills insects close to plants, and interferes with insect larval feeding on such plants. It also prevents insects from colonising host plants and releasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of hypersensitive response elicitor polypeptide - for application to plants or seeds or transgenic plants or seeds for the control of insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This DNA sequence comprises an open reading frame that encodes a hypersensitive response elicitor (HRE) (see AAW75865 of Pseudomonas solanacearum. The invention relates to the use of a HRE
                                                                                                                                                                                                            solanacearum hypersensitive response elicitor DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1035;
                                                                                                                                                                                                                                             insect resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1035 BP; 227 A; 330 C; 368 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ohytotoxins which result in disease damage to plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37.6; DE
Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                          biological control; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 15; 75pp; English.
                                                                                                                                                                                                                                             elicitor;
                                                                                                         AAV54609 standard; DNA; 1035 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.3%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0039226.
                                                                                                                                                                                                                                                                                                                                                                                         98WO-US03604
                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                          seudomonas solanacearum
                                                                                                                                                                                                                                          Aypersensitive response
                              832 aagggtgccggc 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-495374/42.
331 ggcggcaacgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zitter TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW75865.
                                                                                                                                                                          07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-1998;
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                                                                                                                                                                                                                                                                                                                       W09837752-A1
                                                                                                                                                                                                          Pseudomonas
                                                                                                                                                                                                                                                                                                                                                        03-SEP-1998
                                                                                                                                          AAV54609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wei Z,
                                                                                          AAV54609
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Wethod for enhancing plant growth - comprises use of hypersensitive response elicitor polypeptide or protein which may also effect, e.g. increase in plant height or earlier germination seed

(CORR) CORNELL RES FOUND INC

Wel Z;

WPI; 1998-427940/36. P-PSDB; AAW62457. Beer SV, Qiu D,

98WO-US01507.

27-JAN-1998; 27-JAN-1997;

30-JUL-1998

Hypersensitive response elicitor; HRE; growth; transgenic plant;

Pseudomonas solanacearum.

W09832844-A1

Pseudomonas solanacearum hypersensitive response elicitor DNA

09-NOV-1998

AAV39975;

AAV39975 standard; DNA; 1035 BP

RESULT 11 AAV39975

832 aagggtgccggc 843

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This DNA sequence comprises an open reading frame that encodes a hypersensitive response elicitor (HEE) (see AAWG5457) of pseudomonas solanacearum. A method of enhancing growth in plants comprises:

(a) applying a HRE polypeptide or protein in a non-infectious form to a plant or plant sed under conditions effective to enhance or growth of the plant or plants grown from the seed, or (b) providing a transgenic plant or plant sed transformed with a DNA molecule conditions at a plant produced from the transgenic seed under conditions effective to enhance plant growth. HRES (see AAW65454-59) or nucleic acids (see AAV65454-57) encoding them can be used to increase plant growth. THE RES may also result in increased plant height and growth, and effect early germination and maturation of plant seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 aacggtcaacaggaaggcctgagtccgttgacgcagatgcgatgcagatcgtgatgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          712 agcgaagaccagggcctcaccggcgtgctgcaaaagctgatgaagatcctgaacgcg
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37.6; DB 19; Length Pred. No. 2.7;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1035 BP; 227 A; 330 C; 368 G; 110 T; 0 other;
                                                                                                                                                                                                            Disclosure; Page 21; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.3%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 ggcggcaacgcc 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   832 aagggtgccggc 843
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Indels

59;

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211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270

712 agcgaagaccagggcgtctcaccggcgtgctgcaaaagctgatgaagatcctgaacgcg 771

ctgatgcagaaccagggcggcggcatgggcggtggcggttcggtcaacagcagcctg 330

772 ctggtgcagatgatgcagcaaggcggcctcggcggcggcaaccaggcgaggggggctcg 831

ggcggcaacgcc 342

331

271

g ò g

AAV83991 standard; DNA; 1035 BP.

RESULT 13 AAV83991 AAV83991;

(first entry)

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a coding region for a hypersensitive elicitor protein (HRE, see hAW61115). The invention relates to methods of imparting hypersensitive response induced resistance to plants by treatment of seeds. Isolated HRE polypeptides can be applied to seeds as a means of imparting pathogen resistance to plants grown from the seeds. Alternatively, bacteria containing the gene encoding the HRE can be applied to the plant seeds, or transgenic plant seeds containing a DNA molecule encoding an HRE polypeptide sequences from Erwinia chrysanthemi, are used. HRE polypeptide sequences from Erwinia chrysanthemi, and the montaining a DNA molecule encoding and ARE polypeptide sequences from Erwinia chrysanthemi, and the molecule provided. The methods can impart pelargonii (see AAM61113-18) are provided. The methods can impart environment or pathogenic to the plant seed being treated, or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequence from Pseudomonas solanacearum comprises
                                                                                                                                                              Hypersensitive response elicitor; transgenic plant; seed; pathogen resistance; disease resistance; crop protection; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1035 BP; 227 A; 330 C; 368 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Imparting pathogen resistance to plants - by applying hypersensitive response elicitor polypeptide to seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 24-25; 85pp; English.
                                                                                                                                 Hypersensitive response elicitor DNA.
                                AAV36430 standard; DNA; 1035 BP.
                                                                                                                                                                                                                                                                                                                                                                              (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                 96US-0033230.
                                                                                                                                                                                                                                                                                                               97WO-US22629
                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Wei Z;
                                                                                                                                                                                                                 Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-332931/29.
                                                                                                                                                                                                                                                                                                                                                                                                               Beer SV, Qiu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW61116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adjacent plants.
                                                                                                                                                                                                                                                                                                               04-DEC-1997;
                                                                                                                                                                                                                                                                                                                                              05-DEC-1996;
                                                                                                 26-OCT-1998
                                                                                                                                                                                                                                                                               11-JUN-1998.
                                                                AAV36430;
 12
RESULT 1
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ö 211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270 712 agcgaagaccagggcgctcaccggcgtgctgcaaaagctgatgaagatcctgaacgcg 771 Gaps ö DB 19; Length 1035; 59; Indels 11.0%; Score 37.6; DB 55.3%; Pred. No. 2.7; ive 0; Mismatches Best Local Similarity 55.3 Matches 73; Conservative 331 ggcggcaacgcc 342 aagggtgccggc 843 Query Match ŏ g ò g ð

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Gaps

Indels

Length 1035;

DB 20;

Score 37.6; DI Pred. No. 2.7; 0; Mismatches

11.0%; 55.3%;

73; Conservative

g ò 셤 ŏ

Query Match Best Local Similarity Matches 73; Conserva

831

331 ggcggcaacgcc 342 aagggtgccggc 843

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The present sequence encodes a hypersensitive response elicitor protein (also called hairpin protein) that is able to elicit a hypersensitive response in plants. The specification also describes hypersensitive response elicitors from other pathogenic organisms. The protein, in non-infectious form, is applied to plants to impart disease resistance (to a wide range of viral, bacterial and fungal pathogens), to improve growth (yield, quantity and quality of seeds, to provide earlier germination etc.) and to control insects (e.g. corn borers, Lepidoptera larvae etc.) The same results are provided by transgenic plants expressing the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fragments of an Erwinia hypersensitive response elicitor protein and related DNA - used to impart disease resistance to plants, to increase their growth and to control insects
                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= Hypersensitive_response_elicitor_protein
                                                                     Hypersensitive response elicitor protein; hairpin protein; disease resistance; seed quality; insect control; corn borer; Lepidoptera larvae; transgenic plant; ss.
DNA encoding a hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1035 BP; 227 A; 330 C; 368 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 16-17; 94pp; English.
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1..1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORR ) CORNELL RES FOUND INC
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                                                                                                                                                                                                                               Pseudomonas solanacearum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laby RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW87641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beer SV,
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/*tag= a /product= "hypersensitive response elicitor protein"

WO200020452-A2.

Location/Qualifiers

Pseudomonas solanacearum.

Hypersensitive response; insect control; disease resistance; hypersensitive response elicitor; plant growth; vegetable; crop; ornamental plant; ss.

DNA encoding a hypersensitive response elicitor protein.

08-AUG-2000 (first entry)

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The patent discloses a method to impart stress resistance to plants by applying a hypersensitive response elicitor in a non-infectious form to a plant or seed. The present sequence is a DNA encoding hypersensitive response elicitor protein from Pseudomonas solanacearum. The present sequence is used to transform transgenic plant or plant seeds to impart stress resistance.
                                                                                                     Pseudomonas solanacearum hypersensitive response elicitor encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application of a hypersensitive response elicitor protein to plants impart stress resistance
                                                                                                                                  Hypersensitive response elicitor; environmental stress resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1035;
                                                                                                                                                                                                  Location/Qualiflers
1..1035
/*tag= a
/product= "Hypersensitive response elicitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1035 BP; 227 A; 330 C; 368 G; 110 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37.6; DB 21;
Pred. No. 2.7;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 28; 84pp; English.
                          AAD00674 standard; DNA; 1035 BP.
                                                                                                                                                                                                                                                                                                                                                                           (EDEN-) EDEN BIOSCIENCE CORP.
                                                                                                                                                                                                                                                                                                                        99WO-US26039
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Best Local Similarity 55.3%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                  98US-0107243
                                                                             (first entry)
                                                                                                                                                                         Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                     Schading RL;
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-376566/32.
P-PSDB; AAY71099.
                                                                                                                                                                                                                                                                    WO200028055-A2
                                                                                                                                                                                                                                                                                                                                                  05-NOV-1998;
                                                                            08-SEP-2000
                                                                                                                                                                                                                                                                                                                       04-NOV-1999;
                                                                                                                                                                                                                                                                                              18-MAY-2000.
                                                   AAD00674;
                                                                                                                                                                                                                                                                                                                                                                                                      Wei Z,
RESULT 14
            AAD00674
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Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plants, especially vegetables and ornamental flowers -

Fan H, Niggemeyer JL;

Wei Z,

WPI; 2000-303745/26. P-PSDB; AAY84860.

(EDEN-) EDEN BIOSCIENCE CORP.

98US-0103050. 99WO-US23181.

05-0CT-1999; 05-OCT-1998;

13-APR-2000.

Disclosure; Page 29-30; 100pp; English.

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polypeptide. The specification discribes hypersensitive response elicitor polypeptide fragments, which do not elicit a hypersensitive response elicitor polypeptide fragments, which do not elicit a hypersensitive response. Instead, the proteins impart disease resistance to plants, enhance plant growth, and/or control insects. The polypeptide fragments may be used to these properties to plants. The plants which may be treated in this way include vegetables, crops and ornamental plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower, cendive, cabbage, bussel sprout, bear, parsnap, turnip, caulflower, endive, cabbage, bussel sprout, beet, parsnap, turnip, calificower, corrot, squash, pumpkin, zucchini, cucumber, apple, pear, melon, citrus, strawberry, grape, raspberry, pineapple, soybean, tobacco, tomato, sorghum or sugarcane, Arabidosis thaliana, Saintpaulia, petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia.
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55.3%; Pred. No. 2.7;
ive 0; Mismatches 59;
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Best Local Similarity 55.3
Matches 73; Conservative
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Indels

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AAA14944 standard; DNA; 1035 BP

RESULT 15 AAA14944 ID AAA1 XX AC AAA1

AAA14944;

Search completed: June 28, 2002, 11:25:04 Job time: 3736 sec

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,254
FILING DATE: 10-JUL-1997
FILING DATE: 10-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Hypersensitive Response TITLE OF INVENTION: Induced Resistance In Plants NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESSE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
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Pred. No. 0.19;
                                                                                     05-07-951-715A-4
05-08-459-448A-2
05-08-459-48A-4
0S-08-459-595A-4
US-08-459-595A-4
US-08-459-595A-4
US-08-459-504B-2
US-08-459-504B-2
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NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 14603/10050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/475,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08891254 Patent No. 5776889 GENERAL INFORMATION:
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55.3%;
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 55.5.
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U.S.A.
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US-08-891-254.-8
                                        US-08-891-254-8
Appli
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Sequence 1132,
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Sequence 67
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Patent No. 5
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	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	June 28, 2002, 10:22:23; Search time 39.55 Seconds (without alignments) 2124.062 Million cell updates/s
Title: Perfect score: Sequence:	US-09-829-124-1 342 1 atggactctatcggaaacaagcagcctgggcgaacgcc 342
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	383533 seqs, 122816752 residues
Total number of	Total number of hits satisfying chosen parameters: 767066
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTuG.COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTuG.COMB.seq:*

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:*

SUMMARIES

US-08-425-069-1 US-08-317-844B-1 US-09-103-840A-2 US-08-998-416-1132 US-09-292-768-69 US-08-276-452A-72 US-08-798-744-72 US-09-030-270A-8 US-08-984-207-8 US-09-013-587-8 US-08-949-155-5 US-08-881-784-8 US-09-292-768-3 PCT-US96-08819-8 US-09-292-768-67 5273901-6 ВВ Query Match Length 1665 1665 1665 1665 543 1995 1995 37.6 37.2 37.2 Result Š

US-09-056-556-221

-09-253-691-3

US-08-317-844B-3 -08-425-069-3

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                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            ZIP: 14603
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                                                            RESULT 3
JS-09-030-270A-8
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211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270
                    772 CTGGTGCAGATGATGCAGCAAGGCGGCCTCGGCGGCGCAACCAGGCGCAGGCGCGGCTCG 831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NDTA:
APPLICATION NUMBER: US/08/819,539
FILING DATE: 17-MAR-1997
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Hypersensitive Response
TITLE OF INVENTION: Induced Resistance In Plants
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55.3%; Pred. No. 0.19;
tive 0; Mismatches 59;
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Clinton Square, P.O. Box 1051
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                                                                                                                                                                                                                                                                Sequence 8, Application US/08819539
Patent No. 5859324
GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (716) 263-1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 1035 base pairs
nucleic acid
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Best Local Similarity
Matches 73; Conserv
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US-08-819-539-8
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271 ctgatgcagaaccagggcggcggcatgggcggtggcggttcggtcaacagcagcctg 330
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                                                                    APPLICANT: Zitter, Thomas A.
APPLICANT: Wei, Zhong-Min
TITLE OF INVENTION: INSECT CONTROL WITH A
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
                                                                                                                                                                                                                       E: Nixon, Hargrave, Devans & Doyle LLP
P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,270a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
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Pred. No. 0.19
0; Mismatches
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Sequence 8, Application US/09030270A Patent No. 5977060
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                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Goldman, Michael L. REGISTRATION NUMBER: 30,727 REFERENCE/DOCKET NUMBER: 19 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.3%;
Matches 73; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1035 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qiu, Dewen
Wei, Zhong-Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: single
                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 ggcggcaacgcc 342
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APPLICANT: Q1u, De
APPLICANT: Wei, Z1
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Best Local Similarity
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                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; DB 4; Length 1035; 0.19;
                                             SEED TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Qiu, Dewen
APPLICANT: Wei, Zhong-Min
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS
                                                     NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES: NISON, Hargrave, Devans & Doyle LLP
STREET: P.O. Box 1051, Clinton Square
CITY: Rochester
                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,207
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ADDRESSE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                       HYPERSENSITIVE RESPONSE RESISTANCE IN PLANTS BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 37.6; DE
Pred. No. 0.19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN, MIChael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1201
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,230
FILING DATE: 05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-013-587-8; Sequence 8, Application US/09013587; Patent No. 6277814
                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-984-207-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.0%;
55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (716) 263-1304
       Beer, Steven V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1035 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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Best Local Similarity 55.33
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid_STRANDEDNESS: single
                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 ggcggcaacgcc 342
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APPLICANT: Beer, St
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                               New York : U.S.A.
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                14603
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                                                                                                                                                                COUNTRY:
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211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772 CTGGTGCAGATGATGCAGCAGGCGGCCTCGGCGGCGGCAACCAGGCGCAGGGCGGCTCG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37.6; DB 4; Length 1035;
Pred. No. 0.19;
0; Mismatches 59; Indels 0
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GENERAL INFORMATION:
APPLICANT: Cornell Research Foundation, Inc.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE INDUCED
TITLE OF INVENTION: RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                          SOFTWARE: PATENTING PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/^^^
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Nixon, Hargrave, Devans & Doyle LLP Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                               NAME: GOLDMAN, MICHAEL L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1501
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,048
FILING DATE: 27-JAN-1997
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,775
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOLECULE TYPE: DNA (genomic) 35-09-013-587-8
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l Similarity 55.3%;
73; Conservative
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READABLE FORM:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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APPLICANT: Lewis, Randolph V.

APPLICANT: Xu, Ming

APPLICANT: Hinman, Michael B.

TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK

TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND A TRANSFORMED CELL

TITLE OF SEQUENCES: 69

CORRESPONDENCE S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 ctgatgcagaaccagggcggcggcggcatgggcggtggcggttcggtcaacagcagcctg 330
                                                                                                                                                                                                                                                                                                                                                                                                                             211 aacggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcag 270
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             712 AGCGAAGACCAGGGGGCGTCACCGGCGTGCTGCAAAGCTGATGAGATCCTGAACGC 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1035;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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0.19;
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                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                     Score 37.6;
Pred. No. 0.
                                   NAME: Goldman, Wichael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/10051
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET WINDER: 1447-106P
FELECOMMUNICATION INFORMATION:
TELECHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/425,069
FILING DATE: 19-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08425069
Patent No. 5728810
                                                                                                             TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1035 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                 11.0%;
ilarity 55.3%;
Conservative
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                       single
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 ggcggcaacgcc 342
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Best Local Similarity
Matches 73; Conserv
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                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22046
                                                                                                                                                                                                                                                                                         PCT-US96-08819-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-425-069-1
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110 agcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagg 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  639 AGGIGCAGGIGCAGCAGCAGCAGCAGCIGGAGGIGCCGGACAAGGAGGACIAGGIGG 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lewis, Randolph V.
APPLICANT: Xu, Ming
APPLICANT: Xu, Ming
APPLICANT: Hinman, Michael B.
TITLE OF INVENTION: ISOLATED DNA CODING FOR SPIDER SILK
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND A TRANSFO
TITLE OF INVENTION: CONTAINING THE ISOLATED DNA, AND PRODUCTS
TORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.9%; Score 37.2; DB 1; Length 2338; 49.5%; Pred. No. 0.33;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Birch, Stewart, Kolasch & Birch STREET: 301 No. 5989894th Washington Street CITY: Falls Church STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                       AUTHORS: Xu, Ming AUTHORS: Lewis, Randolph V. TITLE: Structure of a protein superfiber: ITTLE: drafiline silk JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                         /product= "Nephila cla
dragline silk protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08317844B Patent No. 5989894
                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Nephilia clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 1.2154
OTHER INFORMATION: 4rs
OTHER INFORMATION: drag
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 49.5
Matches 96; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              699 ACAAGGTGCTGGAC 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    290 gegeeggeatggge 303
                                                                     MOLECULE TYPE: CDNA
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OPERATING SYSTEM:
                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7120-7124
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                                                                                                                                                                                                                                                                                                                                                                                 TITLE: draf
JOURNAL: Pr
VOLUME: 87
                                                                                              HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22046
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Gaps

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Db 2543136 CAGCGCAGCAGCCATTCCGCTGGTGAGGATTGCCAAAATCGCGAGCACCACACCGAGC 2543077
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 2543256 TTGGCTACCACCAATGCGAGCGCGACGACCCCCACCACAGAGCCCCACGCGCGGAGAGTAG 2543197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 2543196 CCCGGTGTGGGGTGACGGGGCAATGGCAGGTGCCGGCGCATGGCGCGATCCGCCTGCTGC 2543137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 2543076 ACCTGGCGTGCGCGGGGATCGTCAGTTCCGGGACGAGCTGCACCAGGCGACCGCCGCG 2543017
                                                                                                                                                                  OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 cgccttcggctggctccgagcagcagctggatcagttgctcgccatgttcatcatgatga 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 tgctgcaacagagccagggcagcgatgcaattcaggagtgtgggcaacgaacaaccgcaga 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 acggtcaacaggaaggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagc 271
                                                                                                                                                                                                                                                                                                                                                                                                     32 teggeaacetgeagaegatgggeategggeeteageaacaegaggaetecagecageagt 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                            Score 36.4; DB 4; Length 4
Pred. No. 6.1;
0; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                      ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1132, Application US/08998416
; Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
BAPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.2%;
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pohlmann, Rainer
Steiner, Sabine
                               SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: Philip
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0
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CLASSIFICATION:
                                                  SEQ ID NO 2
LENGTH: 4403765
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US-08-998-416-1132
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519 AGCAGCAGCAGGTGCTGGACAAGGCGGATACGGTGGTCTTGGTGGACAAGGTGCCGG 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               579 ACAAGGAGGCTATGGAGGACTTGGAAGCCAAGGTGCTGGACGAGGAGGATTAGGTGGACA 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639 AGTICCAGGTGCAGCAGCAGCAGCAGCTGGAGGTGCCGGACAAGGAGGACTAGGTGG 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 gcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcc 229
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APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE RÉFERENCE: 24366-20007.00
CORRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 tgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: FROM 1 TO 2338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Nephila clavipes dragline silk protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structure of a protein superfiber: drafline silk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A
                                                                 NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,977
REPERENCE/DOCKET NUMBER: 1447-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATE: Sept.-1990
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..2154 OTHER INFORMATION: /product=OTHER INFORMATION: dragline spublication information:
                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
ORGANISM: Nephilia clavipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS: Ku, Ming AITHORS: Lewis, Randolph V.
                                                                                                                                                                                                        TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2338 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
04-OCT-1994
I: 435
                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 49.5
Matches 96; Conservative
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  FILING DATE: 04
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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JOURNAL: Pro
                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL:
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LENGTH: 1665 base pairs
TYPE: nucleic acid
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                                                                                                                                                                              ; NAME/KEY:
; LOCATION:
US-08-949-155-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                          · LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 gagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccag 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 ggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggc 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 GAGAAGGAGCTGGCGATGCTGGACAAGCTGCTGGAGAAGACGACGGGGGACAGAACCAG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 GCGCTGAAGCAGACGATGGTGTCCTGACGAACTTCGCGCGGTTCCGGGACCAGGAGACG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 ctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcaga 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compositions and Methods for the Generation of Transgenic Animal 5: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/949,155 FILING DATE: Concurrently Herewith
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches . 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: ARNOLD, WHITE AND DURKEE STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/027,338
FILING DATE: 11-OCT-1996
ALOR APPLICATION DATE: US 60/046,094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TAMK:177
PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 5, Application US/08949155
; Patent No. 6271436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Piedrahita, Jorge A
APPLICANT: Bazer, Fuller W
                                                                                                                            INFORMATION FOR SEQ ID NO: 1132;
                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                   ACTION TO THE TOTAL TOTAL TOTAL TARES ON GENOMIC)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                  10.5%;
50.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (512) 418-3000
                                                                                                                                                               LENGTH: 657 base pairs
TYPE: nucleic acid
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hibler, David W. REGISTRATION NUMBER: 47
                                                                                                      919-541-8689
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IOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                               ; ORGANISM: PAG1689UP
US-08-998-416-1132
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FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                        STRANDEDNESS
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                                                                                                        TELEFAX:
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106 tecgageageagetagateagttgetegeeatgtteateatgatgatgetgeaacagage 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 ATAGAGGAGCATGAAGGAGGTGAAGGCCTACCGCGAGGAGCTGGAGGCGCAGCTGGGC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 ggcctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccag
                                                                                                                                                                                                                                                                   Score 36; DB 4; Length 1126;
Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness ADDRESSEE: PLLC
STREET: 1420 Fifth Avenue, Suite 2800
                                                                                                                                                                                                                                                                                                          0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.30
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TELECOMMUNICATION INFORMATION:
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IBM PC compatible
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NAME: Shelton, Dennis K.
REGISTRATION NUMBER: 26,997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B.
APPLICANT: Lupien, Shari L.
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINE
                                                                                                                                                                                                                                                               10.5%;
nilarity 49.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 224-0718
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 8:
                                           : 1126 base pairs
nucleic acid
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411 GTGGGCGCGACATGG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 ggcggcgccggcatgg 301
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                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                         TOPOLOGY: linear FEATURE:
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1420 FORTY: Seattle
                                                              TYPE: nucleic
STRANDEDNESS:
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115
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APPLICANT: Croteau, Rodney B
APPLICANT: Croteau, Rodney B
APPLICANT: Lupien, Shari L
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
TITLE REFERENCE: wan13463
CURRENT APPLICATION NUMBER: US/09/292,768
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER APPLICATION NUMBER: 08/881,784
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PATENTI VET: 2.0
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                                                                                                                                                                                                             85 ATCAAGCAATGGCGAAAACCGAAACCCCAAGAACCTGCCTCCGGGCCCGCCGAAGCTG 144
                                                                                                                                                                                                                                                                       cagetggateagttgetegecatgtteateatgatgatgetgeaacagagecagggeage 174
                                                                                                                                                                                                                                                                                             145 CCGCTGATCGGGCACCTCCACCTCTATGGGGGAAGCTGCCGCAGCACGCGCTGGCCAGC 204
                                                                                                                                                                                                                                                                                                                               175 gatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagt 234
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                                                                                                                                                                                                                                                                                                                                                                                           205 GIGGCGAAGCAGTACGGCCCAGTGGCACGTGCAGCTCGGCGAGGTGTTCTCCGTCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                       265 CTCTCGTCCCGCGAGGCCACGAAGGAGGCGATGAAGCTGGTGGACCCGGCCTGCGGGAC
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                                                                                                                                                      Length 1665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 ggcatgggcggttgggtcggtcaacagcagcctgggcggcaacgcc 342
                                                                                                                                                               Pred. No. 1;
0; Mismatches 158; Indels
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); Mismatches 158;
                                                                                                                                                    DB 3;
                                                                                                                                                      Score 35.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/09292768
; Patent No. 6194185
                                                        ORGANISM: Mentha x piperita IMMEDIATE SOURCE:
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                                                                                                                                                   10.3%;
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Best Local Similarity 45.1%;
Matches 130; Conservative
                                                                                                                                              Query Match 10.3
Best Local Similarity 45.1
Matches 130; Conservative
   single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (19)..(1518)
US-09-292-768-3
          TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
STRANDEDNESS:
                                                                                    US-08-881-784-8
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US-09-292-768-3
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APPLICANT: Lupien, Shari L.
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
TITLE OF INVENTION: LIMONENE HYDROXYLASES
                                                                                                                                                             265 ctctcgtcccgcgaggccacgaaggaggcgatgaagctggtggacccggcctgcgcggac 324
                                                      205 giggcgaagcagtacggcccagiggcgcacgigcagcicggcgaggigtictccgicgig 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagc 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 cogetgategggeacetecacetectatgggggaagetgeegeageaggetggeeage 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaccaggggcgcgc 294
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OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: limonene-3-hydroxylase variant
175 gatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagt
                                                                                                         235 ccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcgcgc
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                                                                                                                                                                                                                   295 ggcatgggcggtggcggttcggtcaacagcagcctgggcggcaacgcc 342
                                                                                                                                                                                                                                                                         325 cggttcgagagcatcgggacgaagatcatgtggtacgacaacgacgac 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 158;
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Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: WSUL 13463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 67, Application US/09292768 Patent No. 6194185 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 45.1
Matches 130; Conservative
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; LOCATION: (19)..(1518)
US-09-292-768-67
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LENGTH: 1665
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                                                                                           APPLICANT: Lupien, Shari L.
APPLICANT: Karp, Frank
TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
TITLE OF INVENTION: LIMONENE HYDROXYLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: limonene-3-hydroxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1). [(1665)
OTHER INFORMATION: computer-generated nucleic acid sequence encoding
OTHER INFORMATION: limonene-3-hydroxylase protein variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.3%; Score 35.2; DB 4; Length 1665; 45.1%; Pred. No. 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 158;
                                                                                                                                                                                         FILE REFERENCE: WSUL13463
CURRENT APPLICATION NUMBER: US/09/292,768
CURRENT FILING DATE: 1999-04-14
EARLIER APPLICATION NUMBER: 08/881,784
EARLIER FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.0
Sequence 69, Application US/09292768
Patent No. 6194185
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                           GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.3
Best Local Similarity 45.1
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                        SEO ID NO 69
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Search completed: June 28, 2002, 11:27:18 Job time: 3895 sec BM488443 pgm2n.pk0 BF414279 UI-R-BJ2-

AZ972907 2M0246M24 AL304774 Tetraodon

BF570046
AJ273961
BM48843
BM48443
AZ972907
CNS0455P
BM3805
BM56085
BM876603
A1366107

39 38.8 38.8 38.6 38.6

BF570046 602186053

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(without alignments)
2877.941 Million cell updates/sec
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                                                                                                           June 28, 2002, 10:21:28 ; Search time 1603.91 Seconds
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                     Compugen Ltd
                                                                                                                                                                                                                                                                                                                       13736207 seqs, 6748477542 residues
                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                   OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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B73805 T2712TR TAM B6560855 EEESTE693 A1366107 ao870603 A1366107 ao870603 A1366107 ao87060.x A4106297 am25h04.y B8619096 B8619096 B6297454 602995610 BF072844 20395510 BF072844 219332 MA AZ537043 AST-2P013 BC855860 102404400 AL261374 Tetraodon AL261374 Tetraodon AL261374 Tetraodon AL261374 Tetraodon AL669315 AL669315 B633649 S227787.5 B6239472 HYSME3002 BH326016 CH230-45K

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37. 37. 37.

AW106297 BB619432 BB619096 BG297454 BI633649 BG299472 BH326016 AI440942

337.8 337.8 337.4 337.2 337.2

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_hum:* em_gss_pln:* em_gss_vrt:*

dp_gss:*

gb_est2:'

em_estro: em_htc:*

qb_est1:

AZ101123 RPCI-23-4 BG929756 etsHEST01 AZ661219 IM0539M10 BI832289 603080137 AU142497 AU142497 BG930118 etsHEST05 AQ919110 RPCI-23-2 AL241091 Tetraodon BI895704 EtESTed23 BF592443 7156c04.x AZ640388 1M0502E21 BF199083 249143 MA AZ337339 1M0068B03 BG562218 EtESTee04 BG417526 HVSMEK001 AZ312601 1M0028104 BB867074 BB867074 Description SUMMARIES A2312601 B6G30118 A0919110 BB867074 A2101123 B16922756 A2661219 B183228 A2661219 B183228 A2661219 B183228 A264038 B18522443 A2640388 A2640388 A263138 A2637333 В Query Match Length 12.2 12.0 11.9 11.9 11.9 11.8 39.8 39.2 39.2 40.4 Result Š. U

RESULT

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em_estin:*

em_estmu:

em_estov em_estpl

			ctone unccimuuz8104 K, DNA sequence.	AZ312601	AZ312601.1 GI:10356717	GSS.	house mouse.	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:	Rodentia;	•	Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.	,M., Rose,M., Rose,R., Stokes,R., Tingev,A., von Niederhausern A.	and Wright, D., Welss, R.	Mouse whole genome scaffolding with paired end reads from 10kb	plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss	University of Utah Genome Center	Rm. 308, Biomedical Polymers Research Bldg. 20 S 2030 F. STC ITT	Tel: 801 585,5606	Fax: 801 585 7177	Email: ddunn@genetics.utah.edu	Insert Length: 10000 Std Error: 0.00	Plate: 0028 row: I column: 04	Seq primer: CACACAGGAAACAGCTATGACC	Class: plasmid ends	High quality sequence stop: 526.	Location/Qualifiers		/organism="Mus musculus"	/strain="C57BL/6J"	/db_xref="taxon:10090"	/clone="UUGCIM0028I04"	/crone_iip= mouse loko piasmid ouccim library"	
AZ312601/c	rocus	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS			TITLE		JOURNAL	COMMENT			,		•		-	•			FEATURES	sonrce						

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Email: klwan@pkrisc.cc.ukm.my
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                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was Mydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gil4732114)pblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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                          /note-"Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
             /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
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0; Mismatches 137;
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Universiti Kebangsaan Malaysia
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Tel: 6 03 8292997
Fax: 6 03 8293249
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Matches 138; Conservative
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Eimeria tenella
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FPCI-23-275E22.TJ RPCI-23 Mus musculus genomic clone RPCI-23-275E22 A0919110
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 571)
                                                                                                                                                                                                                                                                                                                               /note="Vector: Lambda ZAPII; Site_1: EcoRI; Site_2: Xhol Sporozoites were excysted in vitro from E. tenella H occysts, purified by column chromatography and mRNA extracted using a FASTTRACK kit (Invitrogen). cDNA was synthesised and a Uni. ZAP XR library was constructed using cDNA synthesis kit, ZAP-cDNA synthesis kit and ZAP-cDNA Gigapack III Gold cloning kit (Stratagene). The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amplified once through E. coli XL1-Blue
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Unpublished (1999)
Other-GSSS: RPCI-23-275E22.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
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Pred. No. 10;
0; Mismatches 127;
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                                                                                                                            1. 537
/organism="Eimeria tenella"
/strain="Houghton"
/db_xref="taxon:5802"
                                                                                                                                                                                                                                /clone="etsHk077"
/clone_lib="EtH11"
/dev_stage="Sporozoite"
/lab_host="XL1-Blue MRF'"
                                                                                                         Location/Qualifiers
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Matches 118; Conservative
PCR PRimers
FORWARD: T3
BACKWARD: T7
Seq primer: SK.
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12.0%;
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ECORI, Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
BHIOB electrocompetent cells (BRL Life Technologies).

112 c 142 g
                                                      Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seg primer: SP6
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 aacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12; Length 571;
and Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA 7E1: 301 838 0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.2%; Score 41.6; 48.0%; Pred. No. 12
                                                                                                                                                                                                                                                                                                               /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-275E22"
                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                                                                                                                                              Location/Qualifiers
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Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome_res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
AM., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
penese. Genome Res. 10 (10), 1617-1630 (2000)
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawaii, Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute Franciscute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell_line=CRL-1734 SCA-9 clone I5), (strain=BALB/C, cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20-3B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AACTGCAGCAGCACCTCCTGGTCCTCAAGCAGCAGCAGCTCCAGAAGCAGCTCCTGT 110
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Pred. No. 14;
0; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="G4D0005H22"
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289 GCCAGACCAGGASCCAGACCASBHYCCAGACCAGGACCAGACCAGAGCAGGA 230 gotggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagcga 176

117

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g ŏ 셤

177 tgcaaatcaggagtgtggcaacgaacaccgcagaacggtcaacagga

BI895704 425 bp mRNA linear EST 15-OCT-2001 EtESTed23h03.yl Eimeria tenella S5-2 cDNA Neg Selected Elmeria tenella cDNA 5', mRNA sequence.

DEFINITION

BI895704

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CNSO3F0Q 968 bp DNA linear GSS 17-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 021M15 of library G from Tetraodon nigroviridis, genomic survey
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
scale clone-end sequencing, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tetraodontidae; Tetraodon.

1 (bases 1 to 968)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Weissenbach, J.

Firshwater pufferfish Tetraodon nigroviridis

Unpublished
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t 56 others
231 GGCAGCGGGAGCAGCAGCAGCAGGAGGAGCTGGAGAAACAGCGGCTGGAGCAGCAGCTGC 290
                                                                                         aacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtc
                                                                                                                                                                         218 aacaggaaggcctgagtccgttgacgcagatgctgatgcagatgtgatgcagctgatgc
                                                                                                                               171 AGCACCTCAAGCAGCAGCAGGAGATGCTGGCGGCTAAGAGGCAGGAGCTGGAGCAGCAGG
                                                                                                                                                                                                                                                                     278 agaaccagggggggggggggggggggggggggtcggtcaacagcagcctgg 331
                                                                                                                                                                                                                                                                                               291 TCATCCTGCGCAACAAGAAGAAAAAGAGAGAGGCCATCGCCAGCACCAGGGGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="021M15"
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g 218 t
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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/clone_lib="G"
/note="Genoscope sr
... 292 g
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CNSO3F0Q/C
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                    158
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AUTHORS
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/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
; Sporozoites were obtained from in vitro sporulated and
excysted ocysts of E.tenella grown in chickens. CDNA was
synthesized from poly mRNA using an oligo-dT primer
containing a XhoI site. Following second strand synthesis,
EcoNI adapters were ligated to the cDNA and products were
slace-selected on sephacryl S500. The cDNA were ligated to
EcoNI/XhoI prepared lambda Zapii (Stratagene). Clones were
converted to phagemids by mass excision using ExAssist
helper phage and E.coli Solx cell (Stratagene). Clones
were selected by negative hybridization against a pool of
overrepresented ESTS (N>-10, from 1682 previous reads).
Insert sizes range from 1.2-2.9Kb. The library may contain
a small percentage of host or bacterial contaminents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone avallability.
Seq primer: -40RP from Glbco
High quality sequence stop: 391.
Location/Qualifiers
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                                                                                                                                      Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                                                                                                                                                                                Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R., Wilson, R. and Sibley, D. Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 gagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccag 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5802"
/clone_lib="Eimeria tenella S5-2 cDNA Neg Selected"
/dev_stage="Sporozoite stage"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: David Sibley, Ph.D.
WashU-Merck Elmeria tenella project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40.8; DB 10;
Pred. No. 17;
0; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Eimeria tenella"
                   BI895704.1 GI:16138840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain-"LS18"
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51.3%;
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Matches 119; Conservative
                                                                              Eimeria tenella.
Eimeria tenella
                                                                                                                                                                Eimeria.
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Gaps

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72; DB 12;

12.0%; Score 41.2; Di 41.1%; Pred. No. 17; :ive 27; Mismatches

Conservative

Query Match Best Local Similarity Matches 69; Conserv

21

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Length 968;

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PCR PRimers
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Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret .B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhaoétigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pleterédejong.med buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
176 GGCTAGCAGCAGCAGCAGCACCAGCAGCAGCAGCGCCGCTAGCAGCAGCAGCACCAG 235
                                                                   229 ctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg-g 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with a combination of EcoRI and EcoRi Methylase.
                                                                                                                                                                   Length 803;
                                                                                                                                           288 cggcggcatgggcggtggcggttcggtcaacagcagcctggggcgacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Chrbar_GSSs: RRCI-23-478E19.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
711: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40.8; DB 12;
Pred. No. 20;
0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="RPCI-23-478E19"
/clone_lib="RPCI-23"
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Best Local Similarity 46.7
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                           , DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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BG929756 325 bp mRNA linear EST 31-DEC-2001 etsHEST0177 EtH11 Eimeria tenella cDNA clone etsHd066 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 325)
Ng, S.T., Jangi, M.S., Shirley, M.W., Tomley, F.M. and Wan, K.L.
Comparative EST analyses provide insights into gene expression in
two asexual developmental stages of Eimeria tenella
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: Lambda 2APII; Site_1: EcoRI; Site_2: XhoI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sporozoites were excysted in vitro from E. tenella H. Ocoysts, purified by column chromatography and mRNA extracted using a FASTRACK kit (Invitrogen) cDNA was synthesised and a Uni-ZAP XR library was constructed. using cDNA synthesis kit, ZAP-cDNA synthesis kit and ZAP-cDNA Gapack III Gold cloning kit (Stratagene). The library was amplified once through E. coli XIJ-Blue
                                                                                                         70 cacgaggactccagccagcagtcgccttcggctggctccgagcagcagctggatcagttg 129
                                                                                                                                                             130 ctcgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgcaaatcaggag 189
                                                                                                                                                                                                                                                                         132 CAGCAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAGCAGAAG 191
                                                                                                                                                                                                                                                                                                                                 190 tgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgttgacgcagatg 249
                                                                                                                                                                                                                                                                                                                                                                             atcggaaacaacttttcgaatatcggcaacctgcagacgatgggcatcgggcctcagcaa
                                           12 AGCAGCAGCAGCAGTAAGCAGAGCAGCAGCAGCAGTAAGCAGAAGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Centre for Gene Analysis and Technology
Universiti Kebangsaan Malaysia
                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 ctgatgcagatcgtgatgcagctgatgcagaaccag 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43600 UKM Bangi, Selangor DE, Malaysia
Tel: 6 03 8292997
Fax: 6 03 8293249

    .325
    /organism="Eimeria tenella"
/strain="Houghton"

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/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref~"taxon:5802"
/clone~"etsHd066"
/clone_lib="EtH11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: klwan@pkrisc.cc.ukm.my
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Length 325;

Score 40.6; DB 10; Pred. No. 17;

11.9%; 51.5%;

Query Match Best Local Similarity

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Indels

us-09-829-124-1.rst

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Matches 120;
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BI832289
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                                                                                                                                                                                                                                                                                                                                                                                                                                            559 bp DNA linear GSS 14-DEC-200
1M0539M10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0539M10 R, DNA sequence.
AZ661219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 559)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longare, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A.; von Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                        230 tgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagatgcagaaccagg-gc 288
                                         110 agcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagg 169
                                                                                                                               170 gcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcc 229
                                                                                                                                                                            99 AGAGGCAGCAGCAGCAGCGGCACCAGCAACTGCAGCTGCAACAAAAACAGCTGGTGC 158
                                                                 /clone_lib="Mouse 10kb plasmid UUGC1M library
  Indels
                                                                                                                                                                                                                                                                                                                289 ggcgccggcatgggcggtggcggttcggtcaacagcagcctgggcgg 335
                                                                                                                                                                                                                                                                                                                                          Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0539 row: M column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 559.
Location/Qualifiers
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/clone="UUGC1M0539M10"
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Conservative ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid inserts
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of pWD42 (gi|4732114|gb|AFI29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (stratagene) cells and selected for amplialin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI832289 585 bp mRNA linear EST 04-OCT-2001 603080137F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5171817 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: brain; vector: pCMV-SPORT6; Site_1: NotI; Site_2: ECoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov.j column: 10
High quality sequence start: 8
High quality sequence stop: 375.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244
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National Institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               gagcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Thisale Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 ctgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaacca-ggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 cggcgccggcatgggcggtggcggttcggtcaacagcagcctgggcggcaacgcc 342
                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                               Length 559;
                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                         Score 40.6; DB 12;
Pred. No. 20;
0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/clone="IMAGE:5171817"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI832289.1 GI:15943839
                                                                                                                                                                                                                                                                                                                         11.9%;
llarity 51.1%;
Conservative
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B1832289
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Gaps

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Indels

86;

Mismatches

6

Conservative

92;

Matches

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116 agetggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggcagcg 175

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0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NHH MGC Library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                       192 tggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtccgttgacgcagatgct 251
                                                                                                                                                                                                                 cgccatgttcatcatgatgatgctgcaacagagccagggcagcgatgcaaatcaggagtg 191
                                                                                                                                                                                                                                           105 AGGAAGGAGGGTCGGAGGACGACGAGGACAACCAGAGGCCGCTGGAGGACAGCGC 164
                                                                                                                                                                                                                                                                                                                                                             252 gatgcagatcgtgatgcagctgatgcagaaccagggcggcggcggcatgggcggtggcgg 311
                                                                                                                                                                                                                                                                                                                                                                                             165 GACGGAGGCGGAGGAGCCCCCGCGGGTAGCGGAGGAGGCGCAAAGGCCGCGAGGGCGCTC 224
                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU142497 A79AA1 Homo sapiens cDwa clone r79AA1000431.5'
                                                                                                                                                 Length 585;
                                                                                                                                                                                   Indels
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1532–3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
                                                                                                                                           Score 40.4; DB 10;
Pred. No. 22;
0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="retinoblastoma"
/cell_line="Y79"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           r: pME18SFL3"
209 α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Y79AA1000431"
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                                                                                                                                                                                                                                                                                                                                                                                                                                    312 ttcggtcaacagcagcctgggc 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTGTCCTACTGCCCGCTGCGC 246
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                                                                                                                                               11.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81-438-52-3952
                                                                                                                                                                               101; Conservative
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                                                                       138
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                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                               Matches
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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JOURNAL
COMMENT
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KEYWORDS
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Length 815;

6 DB

Score 40.4; I Pred. No. 24;

11.8%; 51.7%;

Query Match Best Local Similarity

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BG417526 "850 bp mRNA linear EST 23-OCT-2001
HVSMEk0017024f Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEk0017024f, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plants were raised from seeds in a Controlled Environments Plants were raised from seeds in a Controlled Environments growth chamber maintained in continuous light at 180c, and testa and pericarp were dissected from developing kernels at Washington State University, Pullman, WA (Kannangara, von Wetstein). Total RNA was prepared, poly(A) RNA was purified, one cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids in the TJ Close lab at the University of California, Riverside (Akhnov, Chin, Chol, Close, Fenton, Chin, Chol, Chol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 850)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Kannangara, G., von Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Kannan, P., Otto, C., Simons, K., Zhang, D., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R. and Main, D. Poetolopment of a genetically and physically anchored EST resource for barley genomics: Morex testa/pericarp cona library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kianian, Otto, Simons, Zhang). Phagemids were plated and
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                                                                                                                                                            371 AGCACAATGACTTTCTGAAGCTGAGAACCATGCTCATGAAAGTGGAGAATGAGGACATGA 430
                                                                                                                                                                                                                                                                             236 cyttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcggcgc 293
                                                                                                                                                                                                                                                                                                                                        176 atgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctgagtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SC 29634, USA
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/lab_host="TJC121"
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Clemson University

    850
    /organism="Hordeum vulgare"
/cultivar="Morex"

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/clone="HVSMEk0017024f"
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Location/Qualiflers
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Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:13323077
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BG417526.1
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LOCUS
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SOURCE
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Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Email: cgapbs-remain.nlh.gov
Tissue Procurement: Dennis Sgroi, M.D., Fristina Cole, M.D., Ph.D.
student, Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                             ö
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vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hòminidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BF592443 2112-DEC-20 7156c04.xl NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338694 3' similar to contains element MSR1 MSR1 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 291)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 tgctgcaacagagccagggcagcgatgcaaatcaggagtgtggcaacgaacaaccgcaga 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 TGAAGCCACAGAAGGAGGCCAGTCGCGTGCATTCGCAGTGGCGGAACGGCGACACTCACA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 acggicaacaggaaggccigagiccgitgacgcagaigcigaigcagaicgigaigcagc 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 tgatgcagaaccagggcggcggcgtgggcggtggcggttcggttcaacagcagcctgg 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 ACTICAAGACGGIGCTCGGCCGGGGAGTTCGGCTCCGTGTACGACGGCTTCTTGGCGG 356
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                                                          Length 850;
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                                                                                                                                                                                                                                                                                                                                       Score 40.4; DB 10;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                       91;
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               info@image.llnl.gov
Seg primer: -40RP from Gibco.
Locatlon/Qualifiers
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
BF592443
BF592443.1 GI:11684767
                                                                                                                                                                                                                                                                                                                                       11.8%;
51.1%;
                                                                                                                                                                                                                                                                                                                                  Ouery Match 11.8
Best Local Similarity 51.1
Matches 95; Conservative
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                                                                                                                                                                                                                                  249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 ATGGCA 362
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carcinoma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel,
average insert size 400 bp. Primary library,
non-amplified. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ640388 605 bp DNA linear GSS 14-DEC-20C 1M0502E21F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0502E21 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLI0-Gold, Ti-resistant, F-"
/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                        111 gcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccaggg 170
                                                                                                                                                                                                                                                                                                                                                   69 GAAGCAGGAGGAGCAGATGCGGAAGCAGGAGCAGATGGGGGGAGCAGGAGGAGCAGAT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                     171 cagogatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcct 230
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                                                                                                                                                                                                                      Length 291;
                                                                                                                                                                                                                                                                 85; Indels
                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0502 row: E column: 21
                                                                                                                                                                                                                   Score 40; DB 1
Pred. No. 23;
0; Mismatches
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    605
    /organism="Mus musculus"

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Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 605
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/clone="UUGC1M0502E21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata;
Hammalia; Eutheria; Rodentia;
1 (bases 1 to 605)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
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                                                                                                                                                                                                                      11.7%;
51.7%;
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AZ640388/c
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oilgonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to 10.5 K range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil4732114|gb|AF129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 agcagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaa&agagccagg 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gcagcgatgcaaatcaggagtgtggcaacgaacaacgcagaacggtcaacaggaaggcc 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgagtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagg-gc 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39.8; DB 12; Length 605;
Pred. No. 31;
0; Mismatches 112; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 51.1%;
Matches 118; Conservative
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ORIGIN
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Search completed: June 28, 2002, 10:50:23
Job time: 1735 sec
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Single pass sequencing. Bases called and alt_trimmed with phred
vo.900904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMETS
                                                         EST 03-NOV-2000
                                                                                                                                                                                                                                                           Smith, T.P.L., Casas, E.,
                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus
                                                                                                                                                                                                                                                                              Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                Design and use of two pooled tissue normalized cDNA libraries EST discovery in swine Unpublished (2000)
                                                BF199083 507 bp mRNA linear 249143 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                           Rohrer, G.A.,
                                                                                                                                                                                                                         1 (bases 1 to 507)
Fahrenkrug, S.C., Freking, B.A., Stone, R.T., Heaton, M.P., Grosse and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: 81 row: N column: 2
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                         BF199083.1 GI:11090834
                                                                                                                                                                      scrofa
                                                                                        BF199083
  BF199083/c
LOCUS
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ACCESSION
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/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                                                                                                 cagcagctggatcagttgctcgccatgttcatcatgatgatgctgcaacagagccagggc 171
                                                                                                                                                                                                                                                                                                                                                            247 CTGGGTCAGCCTCTGCAGCTGGCCGCTCACATCCCTCACAGCGGCCACCAGCTCGACCAG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 GG-CAGGCGCTCACAAGCCATGACCCTTACTGGTGGAGCTGGGGCCTCGCATGGGCCAA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 agtccgttgacgcagatgctgatgcagatcgtgatgcagctgatgcagaaccagggcggc 291
                                                                                                                                                                                                                                                                                                                                                                                              172 agcgatgcaaatcaggagtgtggcaacgaacaaccgcagaacggtcaacaggaaggcctg
                                                                                                                                                                                                     Length 507;
                                                                                                                                                                                                  Score 39.2; DB 10;
Pred. No. 40;
0; Mismatches 128;
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="WARC_2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                  11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 gccggcatgggcggtg 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AGGGGCCTGGGCTCTG 113
                                                                                                                                                                                                                                Matches 127; Conservative
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June 28, 2002, 10:16:03; Search time 23.71 Seconds (without alignments) 534.054 Million cell updates/sec
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584
1 MDSIGNNFSNIGNLOTMGIG.......OGGAGMGGGGSVNSSLGGNA 114
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     747574 segs, 111073796 residues
                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998_DAT: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999_DAT: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000_DAT: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001_DAT: A_Geneseq_032802:* : /SIDS1/gcgdata/geneseq/geneseqp-embl /SIDS1/gcgdata/geneseq/geneseqp-'SIDS1/gcgdata/geneseg /SIDS1/gcgd /SIDS1/gcgd /SIDS1/gcgc/SIDS1/gcgc SIDS1, /SIDS1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					COLUMNICO	
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Result		Query				
So.	Score	Match	Match Length DB	DB	QI .	Description
			, ,			
.	200	7.00	114	77	AAE10807	Xanthomonas camr
7	111	111 19.0	344	18	AAWO6600	Hyporopadation,
٣,	111	19	344	0	2202020	i Avintenaciadin
,	1		***	13	MAM / 2002	Pseudomonas sola
4	111	19.0	344	13	AAW62457	Pseudomonia sola
2	111	. 19.0	344	10	AAWATTIA	The canomonas acres
				1 1	OTTTOUR	uypersensitive i
0	111	19.0	344	20	AAW87641	A hypersensitive
7	111	19.0	344	21	AAY71099	Depth Care Control of the Control of
œ	Ξ	10	777		0.004044	Tacaronomas anto
•	1 :		*	7 7	AA104000	A hypersensitive
ת	111	19.0	344	22	AAE06712	Pseudomonas sola
10	111	19.0	385	. 15	XAR45751	TOO CHICAGO
-				1		ELWINIA AMINITOVOI
†	111	19.0	385	8	AAW06598	Hypersensitive r

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New plant pathogen hypersensitive response elicitor-receptor protein

Erwinia amylovora Erwinia amylovora Hypersensitive res A hypersensitive r	A hypersensitive r Erwinia amylovora Drosophila melanog	Drosophila melanog Xanthomonas campes Xanthomonas campes Hypersensitive res A hypersensitive r	Additionation compessions of the result of t	Transcription fact Transcription fact Cellular transcrip Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Drosophila melanog Brosophila melanog Brosophila melanog Hypersensitive res Erwinia amylovora A hypersensitive r Drosophila melanog
AAW75863 AAW62455 AAW61114 AAW87639 AAW71093	AAY84854 AAE06710 ABB68750 ABB66921	ABB63688 AAW75867 AAW62459 AAW61118 AAW87643	AAY84852 AAW97851 AAY71098 AAY84859 ABB71657 AAB84634 ABB70437	AAKB4883 AAKB4882 AAW40057 ABB65778 ABB62081 ABB62042 ABB6275 AAW96260 AAW71094 AAX71094 AAX84855
19 19 20 21	22 22 23	70 110 110 110 110	222 231 252 252 252 252 252 252 252 252 252 25	10 116 122 22 22 22 22 21 21
403 403 403 403	403 403 318 1366	1594 20 20 20 20 20	2324 424 2328 3190 3275	2414 2414 2414 1728 1778 197 915 447 447
19.0	19.0 19.0 18.2 16.5	16.1 16.1 16.1 16.1 16.1	15.7. 15.7. 15.4. 15.4.	112311123111351113511135111351113511135
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	TD AAE	.v., v., v., v., v., v., v., v., v., v., v.,
		inition of an analy floresti, 114 AR.
		AAE10807;
		Xanthomonas campestris hypersensitive response elicitor protein.
		1
		Franc Parinogen; nypersensitive response elicitor; HRE; stress resistand
		discuss issistantia, biring amployed Hypersensicive response elicitor; harpin; signal transduction: growth enhancement: insert control.
		virucide; fungicide; antibacterial.
		Xanthomonas campestris.
		WO200170988-A2.
		27-SEP-2001.
	×	
		19-MAR-2001; 2001WO-US08728.
		23-MAR-2000; 2000US-191649P. 01-DEC-2000; 2000US-250710P.
Song X, Fan H, Wei WPI; 2001-590177/66. N-PSDB; AAD18127.		(EDEN-) EDEN BIOSCIENCE CORP.
		Fan H, Wei
		ирг; 2001-590177/66. N-PSDB; AAD18127.

WPI; 1997-051614/05.

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might not be treated separately due to cost and avoids the use of infectious agents or environmentally harmful materials. By HRE treatment enhanced plant growth is achieved which includes greater yield, increased quantity of seeds produced, increased percentage of seeds germinated, increased plant size, greater blomass, more and bigger fruits, etc. which results in economic benefit to cultivators. Greater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        understanding the harpin (Erwinia amylovora hypersensitive response elicitor) induced signal transduction pathway in plants. The protein is useful for studying the downstream components of signal transduction pathway in plants which eventually leads to disease resistance, growth enhancement, insect control and stress resistance. Imparting disease resistance to plants through HRE treatment has the potential to treat previously untreatable diseases, treating diseases systemically which
                                                                                                                                                                                                                                                                                                                                                                    (HRE). The plants are made resistant to infection by viruses, bacteria and fungi and are imparted with resistance against environmental stress and insects through HRE treatment. The protein is useful for
                                                                                                                                                                                                                                                                                                                                         receptor in plants for plant pathogen hypersensitive response elicitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    generation from the given plot of plant. The present sequence is
Xanthomonas campestris pv. pelargonii hypersensitive response elicitor
isolated from plants, which upon silencing is used to study plant signal transduction pathways leading to disease resistance and growth enhancement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein which serves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         increased size and enhanced biomass allow greater revenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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bacterium; fungus; pathogen; biological control agent.
                                                                                                                                                                                                                                                                                                 to an isolated
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                                                                                                                                                                                                        Disclosure; Page 18-19; 78pp; English.
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                                                                                                                                                                                                                                                                                        invention relates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 114; Conserv
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                                                                                                                                                                                                                                                                                        The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9639802-A1
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                          \begin{picture}(20,0) \put(0,0){\line(0,0){$1$}} \put(0,0){\line(0,0){$1$
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58 saggntgntgnapakdgnanagandpskndpsksqapqsanktgnvddannqdpmqalmq 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 LLAMFIMMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of hypersensitive response elicitor polypeptide - for application to plants or seeds or transgenic plants or seeds for the control of insects.
                                                                                                                                                                                 The elicitor may be used in a new method istance to plants, by application of the
                                                                                                                                                                                           for imparting pathogen resistance to plants, by application of the elicitor in a non-infectious form to plant cells, by spraying, injection, leaf abrasion, or plant infection with recombinant bacteria (non-infectious to the host plant, e.g. Escherichia coli) expressing the elicitor as a biological control agent, to alllow recombinant protein infiltration into the plant. The method confers virus, bacterium or fungus disease-resistance on crops and
                                                                                                                                                            This sequence represents a hypersensitive response elicitor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas solanacearum hypersensitive response elicitor (HRE)

    with hypersensitive

                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 111; DB 18;
Pred. No. 0.00045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- QGGAGMGGGGSVNSSLGGN 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.000
17; Mismatches
                                                        Imparting pathogen resistance to plants response elicitor polypeptide or protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            biological control; transgenic plant.
                                                                                                                    Claim 13; Page 50-51; 69pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           19.0%;
25.8%;
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                                                                                                                                                                                 Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.0°
Best Local Similarity 25.8°
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas solanacearum
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                                                                                                                                                                                                                                                                                                                                           ornamental plants
                    N-PSDB; AAT49316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAV54609
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                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Length 344; Indels

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polypeptide or protein in a non-infectious form to a plant or plants comprises: (a) applying a HRE polypeptide or protein in a non-infectious form to a plant or plant seed under conditions effective to enhance growth of the plant or plants grown from the seed, or (b) providing a transgenic plant or plant seed transformed with a DNA molecule encoding a HRE polypeptide or protein, and growing the transgenic plant or produced from the transgenic seed under conditions effective to produced from the transgenic seed under conditions effective to enhance plant growth. HRES (see AAW62454 59) or nucleic acids encoding them (see AAV39972-75) can be used to increase plant growth. The HRES may also result in increased plant height and yield, and effect early germination and maturation of plant seed and early colouration of fruit and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 saggntgntgnapakdgnanagandpskndpsksgapgsanktgnvddanngdpmgalmg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 lledlvkllkaalhmqqpggndkgngvggangakgaggggglaealqeleqilaqlgggg 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE------QQLDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 LLAMFIMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is a hypersensitive elicitor (HRE) protein of Pseudomonas solanacearum. The invention relates to methods of imparting hypersensitive response induced resistance to plants by treatment of seeds. Isolated HRE proteins can be applied to seeds as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pathogen resistance; disease resistance; crop protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypersensitive response elicitor; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 111; DB 19;
; Pred. No. 0.00045;
17; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 agaggaggvggaggadgaggaggaggangadggn 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plants - by
polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Imparting pathogen resistance to plants hypersensitive response elicitor polypep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 23-24; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW61116 standard; Protein; 344
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORR ) CORNELL RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-332931/29.
                                                                                                                                                                                                                                                                                                                                  Sequence 344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qiu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV36430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                   This is the amino acid sequence of a hypersensitive response elicitor (HRE) of Pseudomonas solanacearum. The invention relates to the use of a HRE polypeptide or protein to control insects on plants or plants grown from seed treated with HRE. Also claimed is a method of insect control for plants that involves: (a) providing a transgenic plant or seed transformed with a DNA molecule (see AAV34606-09) encoding a HRE polypeptide or protein (see plants produced from the transgenic plants or transgenic plants produced from the transgenic seeds to control insects. HRE prevents direct insect damage to plants by feeding njury. It kills insects close to plants, and interferes with insect larval feeding on such plants. It also prevents insects from colonising host plants and releasing phytotoxins which result in disease damage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 saggntgntgnapakdgnanagandpskndpsksgapgsanktgnvddanngdpmgalmg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 SIGNNFSNIGNLQTM-----QIGPQQHEDSSQQSPSAGSE-----QQLDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 LLAMFIMMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for enhancing plant growth - comprises use of hypersensitive response elicitor polypeptide or protein which may also effect, e.g.increase in plant height or earlier germination seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypersensitive response elicitor; HRE; growth; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas solanacearum hypersensitive response elicitor (HRE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.0%; Score 111; DB 19; Length 344; 25.8%; Pred. No. 0.00045; Live 17; Mismatches 54; Indels 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the deduced amino acid sequence of the hypersensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 14-15; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 20-21; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW62457 standard; Protein; 344 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 19.0
Best Local Similarity 25.8
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas solanacearum.
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N-PSDB; AAV39975.
                                                                                                                                                                                                                                                                                                                                                                                    344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beer SV, Qiu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9832844-A1.
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30-JUL-1998

AAW62457;

AAW62457

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applying to seeds

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                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                             ------ 42
                                                                                                                                                                                                                                                                                                                                                                     43 LLAMFIMMM-----LOOSOGSDANQECG--NEOPONGQOEGLSPLTOMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a hypersensitive response ellcitor protein (also called hairpin protein) that is able to ellcit a hypersensitive response in plants. The specification also describes
means of imparting pathogen resistance to plants grown from the seeds. Alternatively, bacteria containing the gene encoding the HRE can be applied to the plant seeds, or transgenic plant seeds containing a DNA molecule encoding an HRE polypeptide or protein are used. HRE polypeptide sequences from Erwinia chrysanthemi, Erwinia amylovora, Pseudomonas syringae, Pseudomonas campestris prathomonas campestris pelargonii (see AAWGIII3-18) are provided. The methods can impart pathogen resistance without using agents which are harmful to the maniforment or pathogenic to the plant seed being treated, or to
                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fragments of an Erwinia hypersensitive response elicitor prand related DNA – used to impart disease resistance to plants, increase their growth and to control insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypersensitive response elicitor protein; hairpin protein; disease resistance; seed quality; insect control; corn borer;
                                                                                                                                                                                                                                              Length 344;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                         19.0%; Score 111; DB 19; 25.8%; Pred. No. 0.00045; ive 17; Mismatches 54;
                                                                                                                                                                                                                                                                                                        3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                          -- QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 agaggaggyggaggadggsgaggaggangadggn 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 15-16; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease resistance, seed quality, ins
Lepidoptera larvae, transgenic plant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW87641 standard; Protein; 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EDEN-) EDEN BIOSCIENCE CORP.
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                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-070210/06.
N-PSDB; AAV83991.
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                                                                                                                                                                                                                                                         Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                            344 AA;
                                                                                                                                                              adjacent plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09854214-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAY-1998;
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                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW87641:
                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application of a hypersensitive response elicitor protein to plants to
                                                                                                                                                                                                                                        58 saggntgntgnapakdgnanagandpskndpsksqapqsanktgnvddanngdpmqalmq 117
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                --00LDQ 42
                                                                                                                                                                                                                                                                      43 LLAMFIMMM-----LQQSQGSDANQECG--NEQPQNGQOEGLSPLTQMLMQIVMQLMON- 94
           The protein, in non-infectious form, is applied to plants to impart disease resistance (to a wide range of viral, bacterial and fungal pathogens), to improve growth (yield, quantity and quality of seeds, to provide earlier germination etc.) and to control insects (e.g. coborers, Lepidoptera larvae etc.) The same results are provided by transgenic plants expressing the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypersensitive response elicitor; environmental stress resistance; plant.
m other pathogenic organisms is applied to plants to impar
                                                                                                                                                                                      44;
                                                                                                                                                         Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas solanacearum hypersensitive response elicitor.
                                                                                                                                                                                    Indels
                                                                                                                                                        Score 111; DB 20;
Pred. No. 0.00045;
                                                                                                                                                                                                               3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-
                                                                                                                                                                                                                                                                                                                               95 ------QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                  17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 26-27; 84pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY71099 standard; Protein; 344
                                                                                                                                                        19.0%;
25.8%;
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                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        impart stress resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schading RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-376566/32.
                                                                                                                                                                     Local Similarity
                                                                                                              344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 AA;
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                                                                                                                                                                                   40;
                                                                                                               Sequence
                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71099;
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Matches
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Length 344;

DB 21;

Score 111;

19.0%;

Query Match

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us-09-829-124-2.rag

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344 AA;
Sequence
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Query Match

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5;
                                                                       The present sequence represents a hypersensitive response elicitor polypeptide. The specification describes hypersensitive response elicitor polypeptide fragments, which do not elicit a hypersensitive response. Instead, the proteins impart disease resistance to plants, enhance plant growth, and/or control insects. The polypeptide fragments may be used to these properties to plants. The plants which may be treated in this way include vegetables, crops and ornamental plants such as alfalfa, rice, wheat, barley, rye, cotton, sunflower, petado, sweet potato, bean, pea, chicory, lettuce, endive, cabbage, brussel sprout, beet, parship, turnip, cauliflower, broccoll, radish, spinach, onton, garlic, eggplant, pepper, celery, carrent, squash, pumpkin, zucchini, cucumber, apple, pear, melon,
                                                                                                            LLAMFINMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                     44; Gaps
                                                   ---00LDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    petunia, pelargonium, poinsettia, chrysanthemum, carnation or zinnia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypersensitive response elicitor polypeptides useful for imparting enhanced growth, disease resistance and insect resistance to plants, especially vegetables and ornamental flowers
                                                                                                                                                                                                                                                                                                                                                                                                                  Hypersensitive response; insect control; disease resistance;
hypersensitive response elicitor; plant growth; vegetable; crop;
ornamental plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saintpaulia
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strawberry, grape, raspberry, pineapple, soybean, sorghum or sugarcane, Arabidopsis thaliana, Saint
                                              SIGNNFSNIGNLQTM -----GIGPQQHEDSSQQSPSAGSE--
25.8%; Pred. No. 0.00045; ive 17; Mismatches 54;
                                                                                                                                                                                               178 agaggaggyggaggaggaggangadggn 212
                                                                                                                                                                                                                                                                                                                                                                                 A hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 28-29; 100pp; English.
                                                                                                                                                                                                                                                                                    AAY84860 standard; Protein; 344 AA
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                                                                                                                                                                                                                                                                                                                                                    (first entry)
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas solanacearum.
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Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fan H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200020452-A2.
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                                                                                                                                                                                                                                                                                                                     AAY84860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comato,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for producing transgenic plants of the invention. The present sequence is Pseudomonas solanacearum hypersensitive response elicitor protein.
                                                                                            58 saggntgntgnapakdgnanagandpskndpsksqapqsanktgnvddannqdpmqalmq 117
                                                                                                                                                                molecule encoding a hypersensitive response elicitor protein or polypeptide, promoter operably linked 5' to the first DNA molecule to induce transcription of the first DNA molecule in response to activation of the promoter by an oomycete and a 3' regulatory region operably linked to the first DNA molecule. The invention also relates to a transgenic plant resistant to disease resulting from comycete infection, the transgenic plant including the chimeric gene, wherein the promoter induces transcription of the first DNA molecule in
                          44; Gaps
                                                                ---00LDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New chimeric gene, useful for controlling plant-pathogenic fungi and producing oomycete-resistant transgenic plants, comprises first DNA encoding hypersensitive response elicitor, promoter and regulatory
                                                                                                                                  43 LLAMFIMM.----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas solanacearum hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a chimeric gene that includes a first DNA
                          Indels
  ; Pred. No. 0.00045; 17; Mismatches 54;
                                                        3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-
                                                                                                                                                                                                                                                  178 agaggaggygygaggadgaggaggangadggn 212
                                                                                                                                                                                                                  --- QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; crop loss; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 16-17; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                     Æ
                                                                                                                                                                                                                                                                                                                                             AAE06712 standard; Protein; 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORR ) CORNELL RES FOUND INC.
    25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JAN-2000; 2000US-0178565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JAN-2001; 2001WO-US02579.
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
Best Local Similarity 25.89
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas solanacearum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-488791/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beer SV, Bauer DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD12808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155347-A1.
                                                                                                                                                                                                                95 -----
                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                       AAE06712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
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GSDANQ -- ECGNEQPQNGQQ ---- EGLSPLTQMLMQIVMQLMQNGGGAGMGGGGGSVNSSL 110
                                                                                                       5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erwinia amylovora, with a mol.wt. of 37,000. The elicitor has a pI of 4.3, thermostability at 100 deg C for at least 10 min, and contains no cysteine. The elicitor may be used in a new method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   imparting pathogen resistance to plants, by application of the elicitor in a non-infectious form to plant cells, by spraying, injection, leaf abrasion or plant infection with recombinant bacteria (non-infections to the host plant, e.g. Escherichia coli) expressing the elicitor as a biological control agent, to alllow recombinant procein infiltration into the plant. The method confers virus, bacterium or fungus disease-resistance on crops and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a hypersensitive response elicitor from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Imparting pathogen resistance to plants - with hypersensitive response elicitor polypeptide or protein
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypersensitive response; elicitor; Erwinia amylovora; plant; disease-resistance; Escherichia coli; infiltration; virus; bacterium; fungus; pathogen; biological control agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.0%; Score 111; DB 18; 31.5%; Pred. No. 0.00052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 31.5%; Pred. No. 0.00
Matches 39; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            Hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 46-47; 69pp; English.
                                                                                                                                                                                                                                                                                             AAW06598 standard; Protein; 385 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US08819.
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                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erwinia amylovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ornamental plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beer SV, Wel Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAT49314
                                                                                                                                                            111 GGNA 114
                                                                                                                                                                                                 236 dqss 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9639802-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                  AAW06598;
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                                                                                                                                                                                                                                                                         AAW06598
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                             5
                                                                                  Gaps
                                                                --00LDQ 42
                                                                                                                                    LLAMFIMMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HR-elicitor; fire blight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The hrpw gene was isolated from E.amylovora using a 48-fold degenerate oligonucleotide probe corresponding to amino acids 9-15 at the N-terminus of harpin. The 4KD protein encoded by the hrpw gene is a hypersensitive response elicitor protein. The harpin is thought to be an archetype for HR elicitors from phytopathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosaceae; apple; pear; phytopathogenic bacteria; defence reaction; hypersensitive reaction and pathogenicity; hrpN; gene cluster; ds.
                             44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amylovora - and DNA encoding it, useful for developing harpin
inhibitors to prevent e.g. fire blight of fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypersensitive response elicitor protein derived from Erwinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 385;
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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0.00045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "corresponds to CAC codon"
                                                            SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.0%; Score 111; DB 15; Best Local Similarity 31.5%; Pred. No. 0.00052; Matches 39; Conservative 21; Mismatches 48;
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                                                                                                                                                                                                                                        Laby
                                                                                                                                                                                                                 -- QGGAGMGGGGSVNSSLGGN 113
     Pred. No. 0.000
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harpin; hypersensitive response elicitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                              AAR45751 standard; Protein; 385 AA.
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   Best Local Similarity 25.8%; Pr
Matches 40; Conservative 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collmer A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORR ) CORNELL RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erwinia amylovora harpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-035054/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Beer SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erwinia amylovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ55751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-1993;
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AAR45751;

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AAR45751 RESULT

Bauer DW,

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Gaps

16;

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7;

Gaps

Indels 16;

48;

Sequence bacteria

Length 385;

176 gqdgtqgsssggkqptegeqnaykkgvtdalsglmgnglsqllgngglggggggnagtgl 235

q ŏ AAW62455 standard; Protein; 403 AA.

AAW62455

. AAW62455;

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This is the amino acid sequence of a 39 kDa, heat stable
hypersensitive response elicitor (HRE) of Erwinia amylovora. The
invention relates to the use of a HRE polypeptide or protein to
control insects on plants or plants grown from seed treated with HRE.
Also claimed is a method of insect control for plants that involves:
(a) providing a transgenic plant or seed transformed with a DNA
concenie (see AAV54606-09) encoding a HRE polypeptide or protein (see
AAW75862-67); and (b) growing the transgenic plants or transgenic
plants produced from the transgenic seeds to control insects.
Prevents direct insect damage to plants by feeding nigury. It kills
on such plants. It also prevents insects from colonising host
colonisms and releasing phytotoxins which result in disease damage to
176 gqdgtqgsssggkqptegeqnaykkgvtdalsglmgnglsqllgngglgggggggggg1 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of hypersensitive response elicitor polypeptide - for application to plants or seeds or transgenic plants or seeds for the
                                                                                                                                                                                                                                                Erwinia amylovora hypersensitive response elicitor (HRE).
                                                                                                                                                                                                                                                                              Hypersensitive response elicitor; HRE; insect resistance;
                                                                                                                                                                                                                                                                                              biological control; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 9-10; 75pp; English.
                                                                                                                                                         AAW75863 standard; Protein; 403 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORR ) CORNELL RES FOUND INC
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                                                                                                                                                                                                                    07-DEC-1998 (first entry)
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N-PSDB; AAV54607.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          control of insects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zitter TA;
                                                                                                                                                                                                                                                                                                                         Erwinia amylovora.
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                                                        111 GGNA 114
                                                                                    236 dgss 239
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                                                                                                                                                                                         AAW75863;
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enhance plant growth. HRES (see AAW62454-59) or nucleic acids encoding them (see AAV39972-75) can be used to increase plant growth. The HRES may also result in increased plant height and yield, and effect early germination and maturation of plant seed and early colouration of fruit and plants. E. amylovora HRE can be applied to tomato plants to enhance growth without causing disease in that species; this, bacterium is a pathogen of apple and pear but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for enhancing plant growth - comprises use of hypersensitive response elicitor polypeptide or protein which may also effect, e.g. increase in plant height or earlier germination seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the deduced amino acid sequence of the 39 kDa, heat stable hypersensitive response elicitor (HRE) of Erwinia amylovora. A method of enhancing growth in plants comprises: (a) applying a HRE polypeptide or protein in a non-infectious form to a plant or plants grown from the seed, or (b) providing a transgenic plant or plants grown from the seed, or (b) providing a transgenic plant or plant seed transformed with a DNA molecule encoding a HRE plant or polypeptide or protein, and growing the transgenic plant or produced from the transgenic seed under conditions effective to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                          Hypersensitive response elicitor; HRE; growth; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                      Erwinia amylovora hypersensitive response elicitor (HRE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 31.5%; Pred. No. 0.00055;
Matches 39; Conservative 21; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 15-16; 110pp; English.
                                                                                                                                                                                                                                                                                                                 (CORR ) CORNELL RES FOUND INC.
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                                                                                                                                                                                                                                                                             97US-0036048.
                 09-NOV-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-427940/36.
                                                                                                                             Erwinia amylovora.
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                                                                                                                                                                                                                                                                                                                                                     Beer SV, Qiu D,
                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV39973.
                                                                                                                                                                 W09832844-A1
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48; Indels 16;

19.0%; Score 111; DB 19; Length 403; 31.5%; Pred. No. 0.00055; Live 21; Mismatches 48; Indels 16

Conservative

39;

Matches

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Similarity

Query Match Best Local S

57 GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSSL 110

5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56

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176 gqdgtggsssggkqptegeqnaykkgvtdalsglmgnglsqllgngglgggggggagtgl 235
                                                                      57 GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSSL 110
            118 gnnttsttnspldgalginstsgnddstsgtdstsdssdpmggllkmfseim--gslfgd 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypersensitive response elicitor protein; hairpin protein; disease resistance; seed quality; insect control; corn borer; Lepidoptera larvae; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A hypersensitive response elicitor protein.
                                                                                                                                                                                                                                                                                                                                                                                                AAW87639 standard; Protein; 403 AA
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176 gqdgtqgsssggkqptegeqnaykkgvtdalsglmgnglsqllgngglggggggagtgl 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Erwinia amylovora. It is heat stable at 100 degc for at least 10 min, has a pl of approximately 4.3, and contains substantially no cysteine. The invention relates to methods of imparting the proteins resistance to plants by treatment of seeds. Isolated HRE proteins can be applied to seeds as a means of imparting pathogen resistance to plants grown from the seeds. Alternatively, bacteria containing the gene encoding the HRE can be applied to the plant seeds, or transgenic plant seeds containing a NAM molecule encoding an HRE polypeptide or protein are used. HRE polypeptide sequences from Erwinia chrysanthemi, Erwinia amylovora, Pseudomonas syringae, Pseudomonas solanacearum, Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         campestris pv. glycines and Xanthomonas campestris pelargonii (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. amylovora causes disease in apple or pear
However, it elicits a hypersensitive response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              environment or pathogenic to the plant seed being treated, or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Thus, E. amylovora can be applied to tomato seeds to pathogen resistance without causing diseases in plants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypersensitive response elicitor; transgenic plant; seed pathogen resistance; disease resistance; crop protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW61113-18) are provided. The methods can impart pathor resistance without using agents which are harmful to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Imparting pathogen resistance to plants – by applying a hypersensitive response elicitor polypeptide to seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypersensitive response elicitor protein (39 kDa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HRE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the 39 kDa hypersensitive elicitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 18-20; 85pp; English.
                                                                                                                                                                                                                                                                AAW61114 standard; Protein; 403 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0033230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-US22629.
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qiu D, Wei Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-332931/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  out not tomato.
                                                      111 GGNA 114
                                                                                                                    236 dgss 239
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                                                                                                                                                                                                                                                                                                                             AAW61114;
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98WO-US10874 97US-0048109

Wei Z;

(first entry)

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The present sequence represents a hypersensitive response elicitor protein (also called hairpin protein) that is able to elicit a hypersensitive response in plants. The specification also describes hypersensitive response elicitors from other pathogenic organisms. The protein, in non-infectious form, is applied to plants to impart disease resistance (to a wide range of viral, bacterial and fungal pathogens), to improve growth (yield, quantity and quality of seeds, to provide earlier germination etc.) and to control insects (e.g. corn borers, Lepidoptera larvae etc.) The same results are provided by transgenic plants expressing the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fragments of an Erwinia hypersensitive response elicitor protein and related DNA - used to impart disease resistance to plants, to increase their growth and to control insects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 403;
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                                                                                                                                                                                                                     Claim 4; Page 10-11; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 39; Conserva
WPI; 1999-070210/06
                                 N-PSDB; AAV83989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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16;

Indels

48;

21; Mismatches

19.0%; Score 111; DB 19; Length 403; 31.5%; Pred. No. 0.00055;

Query Match
Best Local Similarity 31.5%;
Matches 39; Conservative 2

5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS-

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176 gqdgtqgsssggkqptegeqnaykkgvtdalsglmgnglsqllgngglggggggnagtgl 235 a

111 GGNA 114 | :: 236 dgss 239

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Search completed: June 28, 2002, 10:21:25 Job time: 322 sec

Mon Jul

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Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 3, Appl. Sequence 4, Appl. Sequence 11, Appl. Sequence 2, Appl. Sequence 53, Appl. Sequence 2, Appl. Sequence 11, Appl. Sequence 11, Appl. Sequence 12, Appl. Sequence 12, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 2, Appl. Sequence 11, Appl. Sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
15-08-90-26-7
Sequence 7, Application US/08891254
Patent No. 577689
Sequence 7, Application US/08891254
Sequence 7, Application US/08891254
Sequence 7, Application US/08891254
Septiment No. 57768
TITLE OF INVENTION: Hypersensitive Response TITLE OF INVENTION HYPER FLOPPY GIAR COUNTER READER FORM:
COMPUTER READER FORM:
COMPUTER READER FORM:
COMPUTER READER FORM:
COMPUTER READER FORM:
COMPUTER: BID PRICE TITLE OF RELEASE #10. Version #1.30
SUSPENTING SYSTEM: US/08/891,254
FILLING DATE: 10-010-1997
CLASSIFICATION: 514
- 08 - 85 - 3.00 - 2

- 08 - 931 - 300 - 2

- 09 - 930 - 200 - 2

- 09 - 930 - 200 - 2

- 09 - 930 - 200 - 2

- 00 - 135 - 132 - 2

- 00 - 135 - 132 - 19

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PRIOR APPLICATION DATA:
APPLICATION UNDER: 08/475,775
PILING DATE: UNDER: 08/475,775
PILING DATE: UNDER: 08/475,775
ATTORNEY AGENT INFORMATION:
NAME: GOLdman, HICHAEL L.
RESISTRATION HUMBER: 30,727
REFERENCE/DOCKET WINDER: 14603/10050
TELEPHONE: (716) 263-1604
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
LENGTH: 344 amino acids
TTPE: amino acid
                                                                          June 28, 2002, 10:16:33 ; Search time 13.3 Seconds (without alignments) 209.362 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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584
1 MDSIGNNFSNIGNLQTMGIG......QGGAGMGGGGSVNSSIGGNA 114
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cggn2_Cptodata_7/1aa/5A_COMB.pep:*

cggn2_Cptodata_7/1aa/5B_COMB.pep:*

cggn2_Cptodata_7/1aa/6B_COMB.pep:*

cggn2_Cptodata_7/21aa/6B_COMB.pep:*

cggn2_Cptodata_7/21aa/6B_COMB.pep:*

cgn2_Cptodata_7/21aa/PccTuS_COMB.pep:*

cgn2_Cptodata_7/21aa/PccTuS_COMB.pep:*
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231628 seqs, 24425594 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                     OM protein -
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Sequence 7, N. Sequence 7, N. Sequence 7, N. Sequence 7, N. Sequence 3, N. Sequence 2, N. Sequence 3, N. Sequen

Ouery Match 19.0%; Score 111; DB 1; Length 344; Bost Local Similarity 25.8%; Pered No. 77-6-65; Matches 40; Conservative 17; Mismatches 54; Indels 44;

; TOPOLOGY: linear ; MOLECULE TYPE: protein US-08-891-254-7

178 AGAGGAGGGVGGAGGADGGSGAGGAGGANGADGGN 212

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mei, Ehong-Win
TITLE OF INVENTION: INSECT COURFOL WITH A
TITLE OF INVENTION: INSECT COURFOL WITH A
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: NIXON, HATGERY, DEVANS & DOJE LLP
STREET: New YORK
STREET: New YORK
STATE: NEW YORK
COUNTY IN BY COMPATER PEADABLE FORM:
WEDINH TYPE: REPEPT REPEBY RE-COSS/NS-DOS
SOFTWARE: PEADELLE FORM:
COMPATER PEADABLE FORM:
WEDINH TYPE: REPEBY RE-COSS/NS-DOS
SOFTWARE: PEADELIN RE-LOSS/NS-DOS
                                                                                                         RESULT 3
135-09-030-270A-7
: Sequence 7, Application US/09030270A
: Patent No. 5977060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: (716) 263-160 INPORMATION FOR SEQ ID NO. SEQUENCE CHARACTERISTICS: LENGTH: 344 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-09-030-270A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.0%; Score 111; DB 2; Length 344;
Best Local Similarity 25.8%; Pred. No. 7.7e-05;
Matches 40; Conservative 17; Mismatches 54; Indels 44; Gaps
                                                          58 SAGGNTGNTGNAPAKDGNANAGANDPSKNDPSKSQAPQSANKTGNVDDANNQDPMQALMQ 117
                                                                                                                                                           3 SIGNNFSNIGNLOTM-----GIGPQOHEDSSQOSPSAGSE------QLDQ 42
                                                                                                                              43 LLAMFINDM-----LOOSOGSDANGECG--NEOPONGOGEGLSPLTOMLMGIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE------QQLDQ 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wel, Zhong-Min
TITLE OF INVENTION: Hypersensitive Response
TITLE OF INVENTION: Hypersensitive Response
TITLE OF INVENTION: Houced Resistance In Plants
WHHERPORT OF SQUENCES: 9
CORRESPONDER: ALONG, Margarawe, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
COMPUTER: Rochester ORN:
COMPUTER: READABLE FORM:
KOMPUTER: READABLE FORM:
COMPUTER: INM FC COMPUTER:
MEXING YETE: PLODG/MS-DOS
OSTAMBE: Patent in Release 01.0, Version 01.30
                                                                                                                                                                                                                                               95 -----QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                      178 AGAGGAGGVGGAGGADGGSGAGGAGGANGADGGN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCATION NUMBER: US/08/819,539 NG DATE: 17-MAR-1997 SIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION DATA:
ELICATION NUMBER: 08/475,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ce 7, Application US/08819539
No. 5859124
AL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILLING DATE:
TTORING JATE:
NAME: Goldman, Michael L.
REGISTATION UNDERE: 30.
REFERENCE/DOCKET NUMBER:
FELECOMMUNICATION INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (716) 263-16
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-819-539-7
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CLASSIPICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,226
APPLICATION NUMBER: US 60/039,226
APPLICATION NUMBER: 38-PEB-1997
NAME: GOLDMAN, NICHOBER: SO,227
REGISTRATION NUMBER: 30,227

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58 SAGGNTGNTGNAPAKDGNANAGANDPSKNDPSKSQAPQSANKTGNVDDANNQDPMQALMQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                        118 LLEDLVKLLKAALHMOOPGGNDKGNGVGGANGAKGAGGGGGLAEALQEIEQILAQLGGGG 177
                                                                                                                                                                3 SIGNNFSNIGNLOTM-----GIGPQQHEDSSQQSPSAGSE------QQLDQ 42
                                                                                                                                                                                                                                                                                                                                     43 LLAMFIMM -----LAQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
Query Match 19.0%; Score 111; DB 2; L. Best Local Similarity 25.8%; Pred. No. 7.7e-05; Marches 46; Conservative 17; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 AGAGGAGGGVGGAGGADGGSGAGGAGGANGADGGN 212
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----OGGAGMGGGGSVNSSLGGN 113

----LOGSOGSDANQECG--NEQPQNGQGEGLSPLTQHLMQIVMQLMQN- 94

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TITLE OF INVENTION: HERESONES INDUCED
TITLE OF INVENTION: HERESONES IN PLANTS BY SEED THEATHERT
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCES: 10
CONFINEL ADDRESS: 10
CONFINEL U. S.A.
TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED THEATHERT
STATE: New York
CONFINEL THOUGH OF ALL ADDRESS: 10
CONFINEL IN STATES TO THE CONFINEL THOUGH OF ALL ADDRESS
SOFTWARE: PETENTION TO THE CONFINEL THOUGH OF ALL ADDRESS
SOFTWARE: PETENTION TO NATH.
PRIORISERIATION NUMBER: US 60/03/1201
FILING DATE: HEROMATION: NUMBER: US 60/03/1201
FILING DATE: HEROMATION: NUMBER: US 60/03/1201
FILING DATE: THOUGH OF ALL ADDRESS
SOFTWARE: PARTONINE TO SEC. 1996
FILING DATE: TO SEC. 1996
SOFTWARE: PARTONINE TO SEC. 1996
SOFTWARE: PARTO
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118 LLEDLYKLLKAALHMQQPGGNDKGNGVGGANGAKGAGGQGGLAEALQEIBQILAQLGGGG 177
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25.8%; Pred. No. 7 7e-05;
Live 17; Mismatches 54; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE-------QQLDQ 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
PCT-US96.08819-7
Sequence 7. Application PC/TUS9608819
GENERAL INFORMATION:
APPLICANT: CONTENT CONTEN
COMPUTER: IBM PC COMPACTORS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent: Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWMEE: PatentIL Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 AGAGGAGGGVGGAGGADGGSGAGGAGGANGADGGN 212
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RIDGA APPLICATION DATA:
RIDGATION NUMBER: US 60/036,048
FILING DATE: 27 - 3NN - 1997
ATTORNET/ACBRT NFORMATION:
NAME: GOLOMAN HIGHOLI
REGISTRATION NUMBER: 30,727
                                                                                                                                            RENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 25.8%
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-013-587-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 344 amino aci
TYPE: amino acid
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us-09-829-124-2.rai

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Query Match 19.0%; Score 111; DB 2;
Best Local Similarity 31.5%; Pred. No. 8:9e-05;
                                                                                                                                                                                              111 GGNA 114
                                                                                                                                                                                                                                                                                    58 SAGGNTGNTGNAPAKDGNANAGANDPSKNDPSKSQAPQSANKTGNVDDANNQDPWQALMQ 117
                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 19.0%; Score III; DB 5; Length 344;
Best Local Similarity 25.8%; Pred. No. 7.7e-05;
Matches 40; Conservative I7; Mismatches 54; Indels 44; Gaps
                                                                                                                                                                                                                                         3 SIGNNFSNIGNLOTM-----GIGPQOHEDSSQQSPSAGSE------QQLDQ 42
                                                                                                                                                                                                                                                                                                                                             43 LLAMFINDOM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIYMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARENLI INFORMATION:

APPLICANT: Wel, Zhong Hin

APPLICANT: Wel, Zhong Hin

APPLICANT: Wel, Zhong Hin

APPLICANT: Wel, Zhong Hin

ITILE OF INVENTION: Hypersensitive Response

ITILE OF INVENTION: Induced Resistance In Plants

NUMBER OF SEQUENCES: 9

CORRESONDENCE ADDRESS: 9

CORRESONDENCE ADDRESS: 9

CORRESTE: NILLON Square, P.O. Box 1051

CITY: Rochester

CONFORTE: New York

CONFORTER: NEW YORK

COMPOTER RADABLE FORM:

KEDIN TYRE: PLOPDY disk

COMPOTER INP CCOMPACING

COMPOTER: PLANDALE FORM:

COMPOTER: The PC compacible

OFERATING SYSTEM: PC-DOS/NS-DOS

COMPOTER: 104 PCT NUMBER: 05/08/891,254

FILING DATE: 10-JUL-1997

CLASSIFCATION NUMBER: 08/475,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 AGAGGAGGGVGGAGGADGGSGAGGAGGANGADGGN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08891254
Patent No. 5776889
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-08819-7
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5 CHNFSNIGNL---OTHGI-GPOOHEDSSOOSPS-AGSEQOLDQLLAMFIHMAHLQOS---0 56
1118 GHNTFISTHSELDQAALGHSTSQUDDSTSOSSDPHQQLLAMFEHHA--QSLGD 175
1118 GHNTFISTHSELDQAALGHSTSQUDDSTSOSSDPHQQLLAMFEHHA--QSLGD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 19.0%; Score 111; DB 1; Length 385; Best Local Similarity 31.5%; Pred No. 8.9e-05.
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APPLICARM: Meal, Enon-Min
APPLICARM: Meal, Enon-Min
APPLICARM: Beer, Steven V.
TITLE OF INVENTION: Hypersensitive Response
TITLE OF INVENTION: Induced Resistance In Plants
NUMBER OF SOURENCES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ADDRESSES:
ATTLE OF INVENTION HANGING, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
STATE.
STATE.
COUNTRY: O.S.A.
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236 DGSS 239

Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps

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57 GSDANQ -- ECGNEOPONGOQ ---- EGLSPLTOMIMOIVMOLMONGGGAGNGGGGSVNSSL 110
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19 0%; Score 111; DB 5; Length 385;
Best Local Similarity 31.5%; Pred. No. 8.9e-05;
Matches 39; Conservative 21; Mismatches 48; Indels
                                                                                             SERVING STATES OF SERVING SERV
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COMPUTER: TIRM PC Compatible
OFFRANCE STATEMENT STATEMENT PC-DOS/MS-DOS
SOFFWARE: Detentin Release #1.0, Version #1.30
CHRENT PPLICATION DATA:
APPLICATION UNHER: PCT/US96/08819
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19603/10051
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APPLICATION NUBER: US 08/475,775
FLILIG DATE: 07-7UN-1995
ATTORNEY/ACENT INFORMATION:
NAME: GOLdman, Michel L.
REGISTRATION NUMBER: 30,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGULT 11
18708-200-7244-2
1 Sequence 2, Application US/08200724A
5 Patent No. 584968
5 SERENAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acid
TYPE: amino acid
STRANDPOLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
HOLECULE TYPE: protein
PCT-US96-08819-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
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236 DGSS 239
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            оp
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PCT-US93-0643-2
Sequence 2. Application PC/TUS9306243
Sequence 2. Application PC/TUS9306243
Sequence 3. Application PC/TUS9306243
APPLICANT: Ebong-Hin Wel, David W. Bauer, Steven V. SPLICANT: Benegariang He, and Ron J. Laby.
ITILE OF INVERTION: Elicitor of the Hypersensitive Response in Plants
WOMER OF SEQUENCES: 5
CORRESPONDENCE ADRESS: ADDRESSE: ANAWAK & Associates
STREET: 25 Skycop Drive
COUTTER: Counerticutt
COMPUTER: READABLE FORM:
WEDINT TYPE: Topped 1sk
COMPUTER: Machitosh
COMPUTER: Machitosh
SOFTWARR: Mysticosh
COMPUTER: Microsoft Word 4.0
CORPUTER: POPICATION DATA:
APPLICATION DATA:
TLING DATE: 19930630
                                                                                                                                57 GSDANG--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGAGAGGGGSVNSSL 110
                                            57 GSDANO - ECGNEQPONGOO - - - - EGLSPLTOMLMOIVMOIMONOGGAGAGGGGSVNSSL 110
176 GOOGTQGESSGGRQPPERBEDANYKRÜPTLSGAMGNGLGGLGAGGLGGGGGRNTGL 235
177 GOOGTQGESGGRQPPERBEDANYKRÜPTLSGAMGNGLGGLGAGLGAGGGGGRANGLG 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Indels 16; Gaps
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APPLICATION NUMBER: 907,935
FILLING DATE: 01-701-1992
ATTORNEY AGENT INFORMATION:
NAME: GEORGE M. TARMAX
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: GRF DELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide PCT-US93-06243-2
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57 GSDANQ -- ECGNEQPQNGQQ ---- EGLSPLTQMLMQIVMQLMQNGGGAGMGGGGSVNSSL 110
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OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT PRICATION RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
PRILAME DATE:
FLIANG DATE:
APPLICATION NUMBER: US/09/030,270A
PRILOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION BATA:
APPLICATION SHE SHE FEB-199
ATTONEY/ART INFORMATION:
NAME: Coldman, MIChael L.
REGISTRATION MUMBER: 136.03/1521
REGISTRATION MUMBER: 136.03/1521
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IP: 14603
IP: 14603
IP: 1603
IP: 1603
IP: 1609
IP: 1040
IP: 1050
IP: 1040
IP: 1050
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APLICANT: Wel, Zhong-Min
APLICANT: Collmer, Alan
APLICANT: Collmer, Alan
APLICANT: Leby, Ron
APLICANT: Leby, Ron
TITLE OF INVENTION: ELICITOR OF THE HYPER,
TITLE OF INVENTION: ELICITOR OF THE HYPER,
TITLE OF INVENTION: BLICATOR OF THE HYPER,
TITLE OF INVENTION: TO BE ADDRESSEE: NAMBER OF SEQUENCES: 5
CORRESPONDERS ADDRESSEE: NAMBER OF SECUENCES: 5
THERT: Clinton Square, P.O. Box 1051
CITY: Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08851376A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-030-270A-3
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US-08-851-376A-2
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Best Local Similarity 31.5N; Pred. No. 9.4e-05;
Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GNNFSNIGNL --- OTMGI-GPOOHEDSSQQSPS-AGSEQQLDQLLAMFIMMLQQS---0 56
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Patent No. 597/060
Patent No. 597/060
Patent No. 597/060
APPLICANT: Zitter, Thomas A
PPLICANT: Zitter, Thomas A
PPLICANT: Zitter, Thomas A
TITLE OF INVENTION: UNSECT CONTROL HITH A
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
NUMBER OF SEQUENCES: 10
ADDRESSEE: NIZON: Barginave, Devans & Doyle LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                              NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Navon, Hargrave, Devans & Doyle
STREET: Clinton Square
CITY: Rechester
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/200,724A
23-FEB-1994
N: 530
INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatib
OPERATING SYSTEM: PC-DOS/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / MOLECULE TYPE: peptide US-08-200-724A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 GGNA 114
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US-09-030-270A-3
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48; Indels 16;

05-MAY-1997

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57 GSDANQ--ECGNEQPQNGQQ----EGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 GQDGTQGSSSGGKQPTEGEQNAYKKGVTDALSGLMGNGLSQLLGNGGLGGGGGGNAGTGL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFINMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 19.0%; Score 111; DB 4; Length 403; Best Local Similarity 31.5%; Pred. No. 9,4e-0; Marches 99; Conservative 21; Hismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: 01u, Deven
APPLICANT: 01u, Deven
APPLICANT: 01u, Deven
APPLICANT: Beer, Zhong-Min
APPLICANT: Beer, Steven V
TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS
UNDERS OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: 10
CORRESPONDENCE ADDRESS: 01
CORRESPONDENCE ADDRESS: 02
CORRESPONDENCE ADDRESS: 03
CORRESPONDENCE 
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WEDLUM TYPE: FLOADY disk
COMPUTER: IN PC COMPAILS
COMPUTER: IN PC COMPAILS
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTERIN RATE
APPLICATION NAMER: US/09/013,587
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APPLICATION NUMBER: US 60/036,046
FILING DATE: 27-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 403 amino acids
TYPE: amino acid
                                                                                                                                                                                            ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-984-207-3
INFORMATION FOR SEQ ID NO
SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
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236 DGSS 239
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US-09-013-587-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 GSDANQ -- ECGNEQPQNGQQ ---- EGLSPLTQMLMQIVMQLMQNGGGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 GQDGTQGSSSGGKQPTBGEQNAYKKGYTDALSGLMGNGLSQLLGNGGLGGGGGGGGNAGTGL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 19.0%; Score 111; DB 4; Length 403; Best Local Similarity 31.5%; Pred. No. 9.4e-05; Matches 33; Conservative 21; Mismatches 48; Indels 16;
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APPLICANT:
BEEF, Steven V.
TITLE OF INVENTION: HYPERENSITIVE RESPONSE INDUCED
TITLE OF INVENTION: RESISTANCE IN PLANTS BY SEED TREATMENT
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS
STREET: P. O. Box 1051, Clinton Square
CITY: Rochester
STRTE: New York
COUNTRY: U.S.A.
ZIF: 14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
WEDIOM TYPE: PROPRY disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-08-984-207-3
US-08-984-207-3
Patent No. 6235974
GENERAL INFORMATION:
APPLICANT: Q14, Deven
APPLICANT: Q14, Deven
                                                                                                                                                                                                                                                                                           TELEFAX: (716) 263-1600
INPORMATION FOR EAD ID NO: 2: SEGUENCE CHARACTERISTICS: LENGTH: 403 maino acids TYPE: amino acid STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-851-376A-2
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US-09-013-587-3
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Ouery Match 19.0%; Score 111; DB 4; Length 403; Best Local Similarity 31.5%; Pred. No. 9.4e-05; Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps

111 GGNA 114

236 DGSS 239

Search completed: June 28, 2002, 10:21:52 Job time: 319 sec

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	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	Run on: June 28, 2002, 10:16:58; Search time 14:36 Seconds (Without alignments) 762.826 Million cell updates/sec	Title: US-09-829-124-2 Perfect score: 584 Sequence: 1 MDSIGNNFSNIGNLOTMCIGOGGAGMGGGGSVNSSIGGNA 114	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 283138 segs, 96089334 residues	Total number of hits satisfying chosen parameters: 283138	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : PIR_71:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID		111 19:0 344 2 S41707 111 19:0 403 2 T08471 96.5 16 5 272 2 CTCEAR	96.5 14.5 15.6 2 C.5348 96.5 15.5 15.6 2 A33106 96 16.4 534 2 A86386	92.5 15.8 3498 2 T22330 90.5 15.5 748 2 H85204	90.5 15.5 748 2 105795	90 15.4 3190 2 89.5 15.3 597 1	88 15.1 2414 2 A54277 87 14.9 663 2 S21912	86 14.7 794 2 TIO519	85.5 14.6 195 2 G83170 85.5 14.6 521 2 A40252	84.5 14.5 915 2 84.15 14.5 915 2	04 14.4 44/ 2 T18447 63 14.2 353 1 ASS615 83 14 2 426 2 ASS615	83 14.2 1102 2 83 14.2 1655 2	25 82.5 14.1 281 2 G84485 5 5000 Marchining pt 6 82.5 14.1 1145 2 T18235 transcription article 27 82.5 14.1 1480 2 \$846440	82 14.0 696 2 81 13.9 660 2

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hypothetical protein F2J7 4 [imported] - Arabidopsis thaliana (Species Arabidopsis thaliana (mouse-ear Cress) (Species Arabidopsis thaliana (mouse-ear Cress) (Species Arabidopsis thaliana (mouse-ear Cress) (Species 10.7-Mar. 2001 - sequence_travision O.7-Mar. 2001 - sequence_travision O.7-Mar. 2001 - sequence_travision O.7-Mar. 2001 - S.; White, O.; Alor Ching, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar. Nature 408, 816-820. 2000 - Sp. 4000 - Sp. 4
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A.Moteoule type: DNA
A.Residues: 1-534 <STO>
A.Cross-references: GB:AED005172; NID:g10092326; PIDN:AAG12737.1; GSPDB:GN00141
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RiverLance as under 22330
A) Reference number: 219549
A) Reference number: 219549
A) Recents preliminary: translated from GB/EMBL/DDBJ
A) Release preliminary: translated from GB/EMBL/DDBJ
A) Release 1-3499 (MILL)
A) Regidues: 1-3499 (MILL)
A) Regidues: 1-3499 (MILL)
A) Regidues: 1-3499 (MILL)
A) Regidues: 1-3499 (MILL)
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C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 18-Feb-2000
C.Accession: 722330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1428 QQQQQQQHMGPGANNNQMQQLLQQ-----QQSGGG-----GNMAASQMQMTSMH-MT 1474
                                                                                                                                                                                                                                                                                       Ouery Match 16.5%; Score 96.5; DB 2; Length 1596; Best Local Similarity 28.8%; Pred. No. 0.23; Matches 32; Conservative 7; Mismatches 39; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            436 ОННОООООООООООООНОГГОГОНН----ОООООАЅРГИОМОООТЅРГИОМОООТЅРГИ 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 QQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 QQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQQEGLSPLT
A.Cross references; GB.X54251; NID:g8203; PIDN:CAA38152.1; PID:g8204
A.Mores train Canton S
C.Genetics: Tybase.mer
A.Genetics: Tybase.mer
A.Genetics: Tybase.mer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1475 QTQQQITMQQQQFVQSTTTTHQQQQMMQMGPGGGGGGGGGGGSANNNGG 1525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.4%; Score 96; DB 2;
Best Local Similarity 34.1%; Pred. No. 0.077;
Marches 31; Conservative 4; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 OMLMOIVMOLM -----ONOGGAGMGGGG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 QMQQQQQQQQQWVMGGQAFAQAPGRSQQGGGG 522
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A; Map position: 1
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Cispedies: Deinococus radiodurans
Cispedies: Deinococus radiodurans
Cibtei 03-Dec-1999 sequence_revision 03-Dec-1999 $text_change 31-Mar-2000
CiAccession: C15548
RiWhite, O.; Eisen, J.A.; Beidelberg, J.F.; Bickey, E.K.; Peterson, J.D.; Dodson, R.J.;
W.; Shen, M.; Vanahtevan, J.J.; Lan, P.; McDonaid, L.; Utterback, T.; Zalewski, C.; ME
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A.; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RI.
A.; Reference number: A75250; MUID: 20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
|Molecula type: DNA
| Residues: 1.272 <WHIS
| Cross-references: GB:AEO01882; GB:AEO0513; NID:g6457865; PIDN:AAF09792.1; PID:g645787
| Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title: The Drosophila neurogenic locus mastermind encodes a nuclear protein unusually Reference number: A36391, MUID:91065516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rismoller, D.; Friedel, C.; Schmid, A.; Bettler, D.; Lam, L.; Yedvobnick, B. Senes Dev. 4, 1688-1700, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 GSDANG--ECGNEOPONGOO----EGLSPLTQMLMQIVMQLMQNGGGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 19.0%; Score 111; DB 2; Length 403; Best Local Similarity 31.5%; Pred. No. 0.01019. Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps
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                                                                                                                                                                                      5 GNNFSNIGNL---QTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIMMMLQQS---Q 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDSIGNNFSNIGNLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDA 60
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NyAlternate names: mastermind protein
Species: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
16.5; Score 96.5; DB 2; Length 272;
Best Local Similarity 25.5%; Pred. No. 0.033;
Watches 39; Conservative 15; Mismarches 36; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 IMONOGG----AGMGG--GGSVNSSLGG 112
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A;Molecule type: mRNA
A;Residues: 1-1596 <SMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 GGNA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 DGSS 239
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A, Map position: 1
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Tissical States that the state of the state 
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Species: Caenorhabditis elegans
Date: 18-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
Accession: T26218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       572 NAMNNPNSNTGKQE--GFSSQNPTPNSNQSPSSSSQQRHNLVTGGFPNSPQMQQQQRTMN 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 QECGNEOPQNGQQE-----GLSPLTQMLMQIVMQLMQNQGG-----AGMCGGGS-- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           630 GPT-NILPQNHPHQLQSPHSHGNTPEQQMLHQLLQEMSENGGSVQQQQAFSGQSGSNSNA 688
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 DSIGNNFSNIGNLGTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDAN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 YONMANLITSFGAMGLGPQOIQQRDPQMFQQPILHEPIQGMAQNGFGQQVFFTQMQNQQH 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outery Match 15.4%; Score 90; DB 2; Length 707; Best Local Similarity 26:5%; Pred. No. 0.4; Matches 36; Conservative 7; Mismatches 21; Indels 72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 PSAGSEQQLDQLLAMFIMMALQQSQGSDANQECGNEQPQNGQQEGLSPLTQMLMQIVMQL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 FSNIGNLOT----MGIGPQQ-----SSQQS 31
                                                                                                                                                                                                                                               Ouery Match
15.5%; Score 90.5; DB 2; Length 748;
Best Local Similarity 27.0%; Pered. No. 0.38;
Matches 37; Conservative 18; Mismatches 55; Indels 27;
                                              A;Introns: 205/3; 249/3; 266/1; 337/3; 360/3; 394/2; 425/3; 449/1
A;Note: M7J2.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 POGOAQOQLQQL-----AQOHQ------QQQNSQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Residues: 1-3190 <AKI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 -----VNSSLGGNA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         689 ERNTTASTSNISGGGRA 705
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Prothetical protein AT492550 (imported) - Arabidopsis thaliana
| Special Ata | Ata | Ata |
| Special Ata | Ata | Ata |
| Special A
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Reference number: 215452

Accession: 075795

Residue: 1.746 EBEV.

Realdues: 1.746 EBEV.

Cross-references: EBEL.AL022197

Experimental source: cultivar Columbia; BAC clone M7J2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: DNA
Residues: 1-748 <STO>
Cross-references: GB:NC_001268; NID:97269402; PIDN:CAB81362.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 3369 GOOGHQ--PQGSQISQQQQDQQYRRMQAAQMQQDPTAQGQQNRWG--WPSQ-QQSGAAX 3423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pothetical protein M732.110 - Arabidopsis thaliana
Species: Arabidopsis thaliana (mouse-ear cress)
Date: 09-Apr-1999 *sequence_revision 09-Apr-1999 *text_change 13-Aug-1999
Accession: pr 105795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      572 NAMINIPINGNIGKQE--GESSONPIPINSNGSPSSSSQRHULVIGGFPNSPDMQQQQRTWN 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 QECGNEQPQNGQQE-----GLSPLTQMLMQIVMQLMQNQCG-----AGMGGGGS-- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 GPT-NILPQNHPHQLQSPHSHGNFPEQQMLHQLLQEMSENGGSVQQQQAFSGQSGSNSNA 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 GPOQHEDSSQQSPSAGSEQQLDQLLAMFIMMIQQSQGSDANQECGNEQPQNGQDEGLSP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 15.5%; Score 90.5; DB 2; Length 748; Best Local Similarity 27.0%; Pred. No. 0.38; Matches 37; Conservative 18; Mismatches 55; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DSIGNNFSNIGNLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDAN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                Query Match 15.8%; Score 92.5; DB 2; Length 3498; Best Local Similarity 37.6%; Pred. No. 1.3; Matches 32; Conservative 4; Mismatches 42; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3424 SNOMOFOGVRGGOGMG--GMGGSG 3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 LTOMLMOIVMOLMONOGGAGMGGGG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 -----VNSSLGGNA 114
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A;Gene: AT4g25520
A;Map position: 4
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A;Residues: 1-3190 caKI> A;Cross-references: EMBL:U88570; NID:g1916939; PID:g1916930; PIDN:AAB53050.1

A; Map position:

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"Molecule type: mRNA"

Molecule type: mRNA

Molecul
A;Cross-references: SGD:S0001515; MIPS:FKL032c
A;Map position: 1L
C;Map position: 1L
C;Ma
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C.Superfamily: unassigned bromodomain proteins; bromodomain homology
C.Feywords: phosphoprotein: transcription: ainc finger
19.105-1133-70cmain: bromodomain homology agno
F:89.507,1136,1295,1497,1816.1377,2052,320/Shioting site: phosphate (Ser) (covalent)
F:1734/Binding site: phosphate (Ser) (covalent) (by protein kinase A) **status predict
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Title: Molecular cloning and functional analysis of the adenovirus ElA-associated Reference number: A5477; WIID:95011587
Accession: A54277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Newsome, D.; Gerdes, M.; DeCaprio, J.A.; Lawrence,
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|sion: A44277; 860344
| R.; Bzen, W.; Decaptio, U.; Gerdes, M.; DeCaptio, J.A.; Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2132 NWNPWOAGVORAGLPQQQPQQQLQPPMGGMSPQAQQMNMNHNTMPSQFRDILRRQQMMQQ 2191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 QQQQQQQQAPYQGHFQQSPQQQQQNVYYPLPPQSLTQPTSQSQQQQQQQQQQQANSNSNS 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 DSIGNNFSNIG---NLQTMGI--GPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQ 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 DASNSNLLNIGQDHSLQYQGLEHNDSQYRDASHQTP----HQYLMQPQAQPQQQQQQQQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 NLQTMGIG------LLAMFIMMML 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 15.38; Score 89.5; DB 1; Length 597; Best Local Similarity 38.18; Pred. No. 0.38; Matches 36; Conservative 14; Mismatches 59; Indels 1
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Molecule type: protein
Residues: 552-660 <LUN>
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mitted to the Protein Sequence Database, March 1994

Macsasion: 537334

Accession: 537349

Molecule type: DNA

Residues: 1.597 CRIES

Cross-reference: EMB::228032; NID::9486033; PIDN:CAA81867.1; PID::9486034; GSPDB:GN0001

Experimental source: strain 5288C

Experimentals ource: strain 5288C

Experimentals ource: strain 5288C

Burnelle B: 58Ala, J: van Dyck, L:; Tettelin, H:; Goffeau, A.

Burnelle B: 58Ala, J: van Dyck, L:; Tettelin, H:; Goffeau, A.

Reference number: 537851

Reference number: 537851

Reference number: March 1994
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Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new tRNA gene ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      references: EML:X71622, NID:9505182; PIDN:CAB37853.1; PID:94467991
Mental Source: Strain 5288C
S.J.; Kablatt, P.J.; Lippard, S.J.
d to the EMBL Data Library, July S.J.
ption: IXR1, a yeast protein that binds to platinated DNA and confers sensitivity on: 539002
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sidnas; 1-72,74-92,77',94-107,113-206,77',208-219,77T',222-597 <BRO>
sas references; EMBL.15900; NID:9311109; FIDN:AAA02859.1; PID:9311109
mbert, J.R.; Blanchone, V.W.; Cumaky, M.G.
NRII, Acad. Sci. U.S.A. 91,7345-7345, 1994
NRII, Acad. Sci. U.S.A. 91,7345-7345, 1994
ference number: A77793; MUDIO 19316692
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use: 1-527 ccPR5
references: EMBL:228032; NID:g486033; PIDN:CAA81867.1; PID:g486034; GSPDB:GN0001
Imental source: strain 5288C
ile, B.; Skala, J.; Van Dyck, L.; Goffeau, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WA intrastrand crosslink recognition protein - yeast (Saccharomyces cerevisiae)
Alternate names: protein YKL032c; protein YKL245; transcription factor ORD1
Species: Saccharomyces cerevisiae protein 10-sep-1999 *text_change 21-Jul-2000
inde: 10-sep-1999 *text_change 21-Jul-2000
Accession: 837849; 837849; 841668; 839002; AS7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD / 2875 QDAGHGPQHPPQQQQQQVHQQQQQHQH-------HQHQQQGGGGPQQHHPHQQQQQ 2926
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.4%; Score 90; DB 2; Length 3190;
Best Local Similarity 30.1%; Pred. No. 2;
Matches 28; Conservative 6; Mismatches 35; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 QTMGIGPQ -- QHEDSSQQSPSAGSEQQLDQLLAMFIMMALQQSQGSDANQECGNEQPQNG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2927 QQ------VNLMQQQQQGGPGS 2945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 QOEGLSPLTQMLMQIVWQLMQNGGGAGMGGGGS 105
                                                                                                                A/Map position: X
C:Superfamily: bromodomain homology
F:1723-1780/Domain: bromodomain homology <BRO>
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le type: DNA
es: 1-597 <PU3>
C;Genetics:
A;Cross:references: PlyBase:FBgn0015624
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pre-pro-legumin - arrowhead
Species: Sagittaria asgittifolia (arrowhead)
6;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: T10519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 DANOECGNEGPONGG-QEGLSPLTQMLMQIV-----MQLMQNQGGAGMGGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GNNFSNIGNLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQSDANQEC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 D--QETARKLKTSSQEQDGFIIRVERGLQIARPSWRESQEWSQSQSGSGYGTGGQTGPLP 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
14.7%; Score 86; DB 2; Length 794;
Best Local Similarity 29.5%; Pred. No. 1.1;
Matches 36; Conservative 15; Mismatches 53; Indels 18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 GNEQPQNGQQEGLSPL----TQMLMQIVMQLMQNGGGAGNGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565 GOOQQPNGILACSTPKANTPITTQQQMYAAWAAAASASASTSGSANSSLNNS 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A) Accession: T10519
A) Status preliminary; translated from GB/EMEL/DDBJ
A) Status: preliminary; translated from GB/EMEL/DDBJ
A) Residues: 1.794 CCHE>
A) Cross-references: EMEL, F09117; NID:e1008798; PID:e284333
C) Keywords: seed; storage protein
                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.9%; Score 87; DB 2;
Best Local Similarity 28.3%; Pred. No. 0.83;
Matches 32; Conservative 10; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Chen, L.; Fischer, H.
submitted to the EMBL Data Library, October 1996
A;Reference number: 217066
A;Accession: T10519
                                                                           A;Gene: FlyBase:br
A;Cross-references: FlyBase:PBqn0000210
C;Superfamily: POZ domain homology
C;Reywords: zinc finger
F;18-119/Domain: POZ domain homology <POZ>
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Job time: 323 sec
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Pescription: The Drosophila Broad-Complex encodes a family of related, zinc finger-complex encenances and a family of related.
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Special Drosophila melanogaster

Special Structure (1955 sequence_revision 20-Feb-1995 stext_change 01-Dec-2000

Accession: S19193; ASISS_revision 20-Feb-1995 stext_change 01-Dec-2000

Accession: S19193; ASISS_revision 20-Feb-1995 stext_change 01-Dec-2000

Bub Bello, P.; Whithers, D.; Bayer, C.; Fristrom, J.; Guild, G.

To Best EMED Data Library, Angust 1990

Bessription: The Drosophila Broad-Complex encodes a family of related, zinc finger-con-
Reference number: S21911
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Filterio, P.R., Withers, D.A.; Bayer, C.A.; Fristrom, J.W.; Guild, G.W.
Filter: The Drosophila Broad-Complex encodes a family of related proteins containing 21
Filter: The Drosophila Broad-Complex encodes a family of related proteins containing 21
Focesaton: A53235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: D51215
Status: preliminary
Wolcoule type: mRNA
Residues: 1-229,'V',211-663 <DIZ>
Note: sequence extracted from NCBI backbone (NCBIN:79435, NCBIP:79436)
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                                                                                                                                                                                                                                                              e-01-21 protein - fruit fly (Drosophila melanogaster)
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Stross-references: FlyBase:FBgn0000210
Stross-references: FlyBase:FBgn0000210
Steywords: Zinc finger
Sell9/Domain: POZ domain homology <POZ>
11 1
2249 LGAEA 2253
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ues: 1-729, 'V', 231-728 <DI2>
sequence extracted from NCBI backbone (NCBIN:79448, NCBIP:79449)

Mon Jul

Copyrigh	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.		17 90,5 18 90 19 90	15.5	748 377 5	2888
OM protein - protein searc	- protein search, using sw model				531 5	388
Run on: June 28,	June 28, 2002, 10:20:53 ; Search time 22:09 Seconds (Without alignments) 892.776 Million cell updates/sec				3275 5 483 3 1145 4	88488
Title: US-09-829-124-2 Perfect score: 584 Sequence: 1 MDSIGNNFSNIGN	US-09-829-124-2 584 1 MDSIGNNFSNIGNLQTMGIGQGGAGMGGGGSVNSSLGGNA 114				2035 794 10 195 16 642 3	
Scoring table: BLOSUM62 Gapop 10.	BLOSUM62 Gapop 10.0 , Gapext 0.5		31 85.5 32 85 33 85		2994 5 147 5 365 2	688
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Database : SPTREMBL_19:* 1: SP_archea: 2: SP_bacteri. 3: SP_tungi:* 4: SP_humai:*	TREMBL_19:* Sp_arches:* Sp_arches:* Sp_fung:: Sp_fung:: Sp_fung::		45		926 5	a
5: sp_inver. 6: sp_mamma. 7: sp_mbc.*	Sp.intertebrate:* Sp.anmual:sp.anmua	RESULT 09KW32 ID Q	1LT 1 13.2 09KW3.2	PRELIMINARY;	RY;	
	9p_phage:* sp_plant:*	ខ្ពះក្ន	Q9KW32; 01-OCT-2000 01-OCT-2000	(TrEMBLrel. 15,	1. 15, Cr	0.1
	sp_rodent:* sp_virus:*	D D	01-DEC-2001 (HPA1 HOMOLOG	(TrEMBLrel.	1. 19,	7
14: sp_ve 14: sp_un 15: sp_rv	<pre>Sp_vertebrate:* Sp_unclassified:* Dr rvfrus:</pre>	888	Xanthomonas oryzae pv. oryzae. Bacteria; Proteobacteria; gamma	oryzae pv roteobacte	ria; g	2 a a
	sp_bacteriap:•	368	Adhthomonas. NCBI_TaxID=64187	54187;		
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Ogmock arabidopsis

Ografia drasophila

Ografia drasophila

Ografia drasophila

Oggala drasophila

Oggala drasophila

Ogwala drasophila

09kw12 xanthomonas 09z15 xanthomonas 09z15 xanthomonas 09y05 dictyostali 09y05 dictyostali 09w05 dicsophila 09xv6 dicsophila 09xv6 delnocaccus Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Result

PRT; 139 AA.

Ochial H.; Inoue Y.; Hasele A.; Kaku H.;
Construction and characterization of a Xanthomonas oryzae pv. oryzae
baccerial artificial chromosome library.";
FREMS HISTORIAL Lett. 200:59-565(2001).
EMEL: AB043311; BAB07848.1;
SEQUENCE 139 AA; 13727 MM; DDSB57FD8E403898 CRC64; Query Match 32.4%; Score 189.5; DB 2; Length 139; Best Local Similarity 40.7%; Pred. No. 3.5e-13; Marches 50; Conservative 12; Wismatches 49; Indels 13; Gaps 1 MDSIGNNFSNIGNLOTMGIGPOOHED-SSQOSPSAG-SECOLDOLLAMFIMMMLOQS--- 55 . ma subdivision; Xanthomonas group; reated) ast sequence update) ast annotation update)

56 -----QGSDANQECGNEQPQNGQQEGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSSL 110 111 GGN 113 | | |: 118 GGD 120 PRT; 838 AA

us-09-829-124-2.rspt

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58 SAGGNTGNTGNAPAKDGNANAGGANDPSKSQGPQSANKTGNVDDANNQDPMQALMQLLED 117
                                                                                                                                                                                                                                          118 LVKLLKAALHMOOPGGNDKGNGVGGANGAKGAGGGGGLAEALQEIEQILAQLGGGAAGAG 177
                                                                                                                 43 LLAMF-IMMALQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQNQ---- 95
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MEDLINE-99402794; Pubmed-10473630;
MEDLINE-99402794; Pubmed-10473630;
"A novel Ras-Interacting procein required for chemotaxis and cyclic adenosine monophosphate signal relay in Dictyostellum.";
MOL. B104. Cell 10.2829-2845(1999).
SEMEL: AF195241; AAD43567.1; - EAAD911294226808 CRC64;
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Enkaryota; Myestoxoa; Dictyostellida; Dictyostellum.
Nebi_TaxiD-44689;
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01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
RAS INTERACTING PROTEIN RIPA.
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Best Local Similarity 31.29
Matches 39; Conservative
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NCBI_TaxID=305;
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JUINE-0019997; PubMed-10714988;
JUNE-0019997; PubMed-10714988;
J. W., MaChanna M.M., Wiltte F.F.,
Jantification of two novel hrp-associated genes in the hrp gene
Jater of Xanthomonas oryzae by. oryzae.";
Batceriol. 18911844-1853(2000).
JUNE-005199; ANG-051211;
JUNE-005199;
JUNE-0051999;
JUNE-005199;
JUNE-0051999;
J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas oryzae pv. oryzae.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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Bacteria: Proteobacteria; beta subdivision; Ralstonia group;
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32.4%; Score 189; DB 2; Length 143;
Best Local Similarity 41.0%; Pred. No. 4.1s-17,
Matches 50; Conservative 11; Mismatches 49; Indels 1
Matches 50; Conservative 11; Mismatches 49; Indels 1
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19.5%; Score 114; DB 2; Length 330;
Best Local Similarity 28.4%; Pred No. 0.0018;
Matches 40; Conservative 15; Mismatches 56; Indels 3
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Popti Om ( AFR 1997) to the RABL/GenBank/DDBJ databases.
Bani, Agosess, Ban/7797) to the RABL/GenBank/DDBJ databases.
Empiri, Agosess, Ban/77970, 11. REC(2D9E319D4A5 CRC64;
SEQUENCE 310 AA
                                                                                                                                                                                                                  092LJ5 PRELIMINARY, PRT; 143 AA.
092LJ5;
01-MX-1999 (TEMBLRel, 10, Created)
01-MX-1999 (TEMBLRel, 10, Last sequence update)
01-DEC-2001 (TEMBLRel, 19, Last annotation update)
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09WXK0 01WXV-1999 (TERMELRA] 12, Created)
01-WV-1999 (TERMELRA] 12, Last sequence update)
01-WV-1999 (TERMELRA] 12, Last annotation update
POPAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xanthomonas.
NCBI_TaxID=64187;
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NCBI_TaxID-305;
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545 NSSNNSNSSNNNNKKSGGPQPQQSQQQQQQT-----QQTQQ-----TQQQAQQAP 588
                                                                                                                                                                                                                                                                62 QECGNEQPQNGQQEGLSPLTQMLMQIVMQLMQNQ-----GGACMGGGGSV----NSS 109
                                                                                                                                                                                                                                                                                                                10.9%; Score 110.5; DB 5; Length 838; 31.2%; Pred. No. 0.0012; tive 13; Mismatches 38; Indels 35; Gaps
                                                                                                                              2 DSIGNNFSNIGNLOTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDAN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rkholderia solanacearum (Pseudomonas solanacearum).
(Cteria; Proteobacteria; beta subdivision; Ralstonia group;
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56; Indels 30; Gaps

3 SIGNNFSNIGNL QTMGIGPQQH ---- EDSSQQSPSAGSEQQLDQ 42

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REC STRAIN-BERKELEN;
RAY AGMES HE.
RA GARGE W. C. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RAMGHES H.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Hichred S., Ashburner H., Handerson S.N.,
Sutton G.G., Wortnam J.R., Yandell N.D., Zhang O., Chen L.Z.,
RA Stutton G.G., Wortnam J.R., Yandell N.D., Zhang O., Chen L.G.,
RA Stutton G.G., Wortnam J.R., Yandell N.D., Zhang O., Chen L.G.,
RA Brandon R. C., Rogers Y. H.C., Edazej R.G., Champe M., Petiffer B.D.,
RA Ballew R. M., Basu R., Barker B.G., Landers Pefankoch C., Baldwin D.,
RA Ballew R. M., Basu R., Barker M. H. J., Andrews Pefankoch C., Baldwin D.,
RA Berry J.M., Cawley S., Dahke C., Davaport, D., Borites P.,
RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Davies P.,
RA Burtis R.C., Busam D.A., Dahke C., Davaport, D., Davies P.,
RA Grerry J.M., Cawley S., Dahke C., Davaport, D., Davies P.,
RA Grerry J.M., Cawley D., Bernen B.P., Bundart D., Boritar S.M.,
Ra Borson K., Doup L.E., Downes M., Dupan-Roch S., Dubro B.,
RA Godson K., Doup L.E., Downes M., Dupan-Roch S., Dubro B.,
RA Gabrielian A. E., Garrell J., Hernander J.R., Fleschmann W.,
RA Godson K., Doup L.E., Downes M., Dupan-Roch S., Plack M.,
RA Lander S., Raylerian R., Karpen G.H., H., Hennander J.R.,
RA Harris N.L., Harvey D., Helman T.J., Hernander J.R., Flowan C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Lasko P., Lel Y., Leyitaky A.A., Li J., Li Z., Linny Y., Lin X.,
RA Ralson D.E., Knather G.H., Wobarry C., Morris J., Mosheefi A.,
RA Ralson D.M., Pittamn S., Pollad J., Warny D.M., Rang X.,
RA Relson D.M., Pittamn S., Pollad J., Warny D.M., Raylor M.,
RA Relson D.M., Raylon R.A., Nixon K., Waskern D.R., Peciel J.M.,
RA Ralson D.M., Raylon R.A., Nixon K., Waskern D.R., Peciel J.M.,
RA Ralson D.M., Raylon R.A., Nixon K., Wang S., Kang K.,
RA Ralson D.M., Watter D.M., Welssenber D.,
RA Rang Z.-Y., Walk M., Warny D.M., Welssenber D.,
RA Rang Z.-Y., Walk M., Wang S., Rang S., Rang S., Rang S., Rang S., Rang S., Rang S., Rang
                                                                                                    118 LLEDLUKLLKAALHMQQPGGNDKGNGVGGARGAKGAGGGGGLAEALQEIEQILAQLGGGG 177
                                                                                                                                                                                                                            43 LIAMFIMM.----LQOSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0940P3 PRELIMINARY, PRT, 318 AA.
990093 PRELIMINARY, PRT, 318 AA.
01-MAY-2000 (TERMELE1, 13, Last sequence update)
01-DE2-2001 (TERMELe1, 13), Last annotation update)
01-DE3-2001 (TERMELe1, 19, Last annotation update)
                                     3 SIGNNFSNIGNLOTM -----GIGPQQHEDSSQOSPSAGSE-
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When Line 23113006; PubMed-1472716;
Gough C.L., Genth S., Zischek C., Boucher C.A.;
"htp genes of Pseudononas solanacearum are homologous to pathogenicity determinants of animal pathogenicbacteria and are conserved among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEDINE-3302711; PubMed-6316211; Gougher C.A.; Homology between the HrpO protein of Pseudomonas solanacearum and Hidmology between the HrpO protein of Pseudomonas solanacearum and bacterial proteins implicatedin a signal peptide-independent secretion mechanism.;
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WEDLINE-42474349, PubMed-8190064;
Genin S., Boucher C.A.;
"A superfamily of proteins involved in different secretion pathways in gram-negative bacteria: modularstructure and specificity of N-terminal
                                                                                                                                                                                            MEDINE-95349395; PubMed-7623665;
WEDINE-95349395; PubMed-7623665;
Alla Guodin C.L. Zischek C., Genin S., Niqueux E.,
Alla H., Barberts P. Goudin C.L. Zischek C., Genin S., Boucher C.A.;
The hrp gene locus of Feedlomonas solanacearum which controls a type
the fine system, encodes eight-proteins related to components of
the finellar budgenesis complex.;
Moi. Microbiol. 15:1095-1114(1995).
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN-GAILO00;
MEDLINE-3135128; Pubmed=1479894;
Genin S., Gough C.L., Zischek C., Boucher C.A.;
Evidence that the hrps gene encodes a positive regulator of pathogenicity genes from Pseudomonas solanacearum.";
Mol. Microbiol. 6:3065-3076(1952).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dommain.;
Mol. Gener, 243:112-118(1994),
EMBL; AAZ4811; CAB58262.1; -.
SEQUENCE 344 AA; 33152 MW; 42A7C5A0C32B0907 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pathogenic bacteria.";
Plant Microbe Interact. 5:384-389(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Gen. Genet. 239:378-392(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phytopathogenic bacteria.";
Mol. Microbiol. 20:681-683(1996);
MOI. Microbiol. 36:261-277(2000).
[2]
SEQUENCE FROW N.A.
STRAIN-GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Gaps Ouery Match
Best Local Similarity 25.8%; Pred. No. 0.0005;
Matches 40; Conservative 16; Mismatches 55; Indels 44;

SEQUENCE FROM N.A. Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.

us-09-829-124-2.rspt

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MEDLINE-121310; PubMed-11347906;
Magade T., Wakayama M., MakAjima D., Kikuno R., Ohara O.;
Magade T., Wakayama M., MakAjima D., Kikuno R., Ohara O.;
Magade T., Wakayama M., MakAjima D., Kikuno R., Ohara O.;
The complete sequences of 100 new cDNA clones from brain which code for large Proteins in vitro. ",
DNA Res. 88-55-56(201).
DNA Res. MS-55-56(201).
SEMEL. MS-56(201).
SEMEL. MS-56(201).
SEQUENCE 1173 AA; 126815 MW; B3E52EDFE7EEE3B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 QOHEDSSOQSPSAGSEQQLDQLLAMFIMMMLQQSGGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 63; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-20036896, PubMed-10567266, Mickey E.K., Peterson J.D., Moddon R.J., Meddenberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Maff D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moddon R.J., Lan H., Liang L., Pamphile W., Crosby W., Shen M., Manthevan J.J., Lan W., McDonald L., Utterberk T., Zalberski C., Mkarova K.S., Aravid L., Daly M.J., Mincon K.W., Fleischmann R.D., Rechum K.A., Nelson K.E., Salzberg S., Smith H.O., Venet J.C.,
                                                     Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
NCB_CART_CARTU-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deinococcus radiodurans.
Bacteris; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBL_TaxID-1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
17.2%; Score 100.5; DB 4; Length 1173;
Best Local Similarity 30.1%; Pred. No. 0.02;
Matches 28; Conservative 12; Mismatches 40; Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Complete proteome.
SEQUENCE 272 AA; 26985 MW; 1BD37805BE73AE35 CRC64;
             Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NAY-2000 (TrEMBLrel. 13, Created)
MAKY-2000 (TREMBLrel. 13, Last sequence update)
01-MAR-2001 (TREMBLrel. 16, Last annotation update)
HYPOTHETICAL 27,0 KDA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40:
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EMBL; AE001882; AAF09792.1; -.
TIGR; DR0201; -.
      001 (TrEMBLrel, 19,
PROTEIN (FRAGMENT).
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 ---GGPGSMQHNPQGPGGPGGLMPGHSPQHQMQQQQQQQMMQQQMMVPQQGVGVGVGMGG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 SAGGNIGNIGNAPAKDGNANAGANDPSKNDPSKSQGPQSANKIGNVDDANNQDPMQALMO 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 ILEDLVKILKAALHMOOPGGNDKGNGVGGANGAKGAGGGGLAEALQEIEQILAQPGGGA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 QSGGSDANQECGNEQP--QNGQGEGLSPLTQMLMQIVMQLMQNQ----------- 96
                                                                                                                                                                                                                                                                                                                                                5 GNNFSNIG-----NLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.9% Score 104.5; DB 2; Length 339; Best Local Similarity 25.7% Pred. No. 0.002; Matches 39; Conservative 17; Mismatches 55; Indels 41; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 LLAMFIMMY-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQ---- 90
., Li P., Liao G., Miranda A., Mungall C.J.,
Paragas V., Park S., Phouanenavong S., Wan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hikich Y., Kanda A., Hasegawa H., Okuno T.;
"popA in Ralstonia solanacearum OE1-1 pathogenic to tobacco.";
Submitteed (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: A803747; BAR84679.1;
SEQUENCE 339 AA; 32807 WW; 613A51A065D3EDC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POPA-OR.
Burkholderia solanacearum (Pseudomonas solanacearum).
Bacteria: Proteobacteria: beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                      Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                     5 GONGGNGGPSSGGGGGGGPNWNPMGGPGCNQHGNWQQMHMSPQHQQQQQMGMM
                                                                                                                                                                                                                                               Query Match 18.2%; Score 106; DB 5; Length 318 Best Local Stailarity 28.5%; Pred. No. 0, 0013. Matches 18. Indels Matches 46; Indels
                       Numoo J. Pacila J. Park S. Phouanenavong
Yu C. Levis S.E. Pubin G.M. Calniker S. Phouanenavong
Submitted (CCT-2001) to the EMEL/GenBank/DDBJ databases.
EMEL. AR004169; ANA/100 II.
EMEL. NV061627; ANA/100 II.
SEQUENCE PROD
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01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-MAY-2000 (TIEMBLrel. 13, Last annotation update)
POPA-OB PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         096JK6 PRELIMINARY; PRT; 1173 AA. 096JK6 010 (TEMBLEL: 19, Created) 01-DEC-2001 (TEMBLEL: 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 AGAGGAGGGVGGAGGSGAGGANGADGGN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 GAGMGGGGSV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 GVGMGGGGVV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ralstonia.
NCBI_TaxID-305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O9RBYO
Q9RBYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
096JK6
ID 096JK6
AC 096JK6,
DT 01-DEC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
Q9RBY0
ID Q91
AC Q91
   $ $ $ $ $ $ $ $ $ $ $
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39; Indels 33; Gaps

7; Mismatches

Matches 32; Conservative

1 09:28:20 2002

Mon Jul

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RX AGENINE—SCRIEE;

RX AGENINE—COLLINES:

RAMARIA-BERKELE;

RAMARIA-BERKELE;

RAMARIA-BERKELE;

RAMARIA-BERKELE;

RAMARIA-BERKELE;

RAMARIA F. EVELOR F. S. L. I. P. N. HOSKINS R. GAILE R. F.

GOOGGE R. A. Lewis S. E. Richards. S. Ashburner M. Henderson S.N.,

SULTON G. G. HORTMAN J. R. Yandell N.D. Zhang O. CHE L.X.,

RAMARIA J. F. William J. R. Yandell N.D. Zhang O. CHE L.X.,

RAMARIA J. R. William J. R. Yandell N.D. Zhang O. CHE L.X.,

RAMAR H. Basu A., Baxandle J. Bayrakteroglu L. Bessley E.N.,

RAMAR H. Basu A., Baxandle J. Bayrakteroglu L. Bessley E.N.,

RAMAR H. S. Dovile C. Baxerer E.G. Hell G. Nelson C. R. Miklos G.L.G.,

RAMAR R. H. Sovile C. Baxerer B. G. Hell G. Nelson C. R. Baldwin D.

RAMAR R. H. Sovile C. Baxerer B. R. Bender D. Brottler P. J.

RAMAR R. H. Sovile C. Baxerer A. Dong B. P. Barkadari D., Bottler P. J.

Cherry J.M. Cavley S. Dahlke C. Davenport L. B. Davids P. J.

Charter A. Dony L. E. Downes M. Dugan Roche S. Dunkov B.C., Dun P. J.

RAMAR R. Durbin R. J. Evangeliza C. C. Ferrar C. Ferrier S. R. Reison M. J. Evangeliza C. Gargellar C. Mandellar R. J. Hellon P. Harris M. H. H. Ibeywan C. J.

RAMAR B. L. Kodira C.D., Kraft C. J. Nel M. H. J. Ibeywan C. J.

RAMAR B. E. Kodira C.D., Kraft C. L. Liang Y. Lin X. Hervilov G. Milshina N. V. Mobarry C. Morris J. Nosheef J. A. Nosheef J. A. Nosheef J. M. Nelson D. L. Mandellar R. Sandels R. R. Sanders R. D. Krapt D. R. Nelson D. L. Mandellar R. Sander R. Sanders R. Scheller F. Shem H. She R. She R. Sheeler F. Shem H. She R. She R. Tector C. Turner R. Venter E. Spander J. W. Nosker R. Sheller R. Sanders R. Wang R. H. Nosker R. Mang X. M. Mang X. M. Wang R. M. R. Mang X. M. Mang R. W. Welson D. R. Welson D. M. Stupski M. B. Sanders R. Wengellar R. Wenge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   904688 PRELIMINARY; PRT; 1366 AA. 094688 OPTELIMINARY; PRT; 1366 AA. 095688.
01-MAY-2000 (TEMBLEAL. 13, Created)
01-MAY-2000 (TEMBLEAL. 13, Last sequence update)
01-MAY-2001 (TEMBLEAL. 16, Last annotation update)
MAM PROTEIN.
MAM ROSEIN.
MAM ROSE
91 LMONOGG------AGMGG--GGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                       139 MGGNMGGQSGGGMSLPGGMGGGLGGGLGSILGG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141456 MW;
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STRAIN-BERKELEY;
MEDLINE-20196006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
0996#8
1D 0996#8
AT 01-WAY.
DT 01-WAY.
DT 01-WAY.
CD NAM OR
CD MAM OR
OS Drosopl
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Adams W.D., Cellibrar S.E., Lil P.W., Hookins C.A., Gocayne J.D.,
RA Adams W.D., Cellibrar S.E., Lil P.W., Hookins R.A., Galle R.F.,
George R.A., Levis S.E., Kichards S., Ashburner W., Henderson S.N.,
Storion G.A., Levis S.E., Krichards S., Ashburner W., Henderson S.N.,
Brandon R.C., Mortman J.R., Yandell M.D., Ehnng O., Chen L.X.,
Rank K.H., Doyle C., Barter B.G., Helf G., Change M., Pfeiffer B.D.,
RA Mar K.H., Doyle C., Barter B.G., Helf G., Nelson C.K., Miklog G.L.G.
Abril J.F., Agbayanl A., An H.-J., Andrews-Pfennicoh C., Baldvin D.,
RA Ballew R.W., Basu A., Barendala J. Bayterkirgjul L., Beasley E.M.,
Resson K.Y., Benca P.V., Berman B.P., Bhindari D., Bolshakoy S.,
RA Burtis K.C., Busan D.A., Barter M. Bouck J. Brottler P., Golshakoy S.,
RA Burtis K.C., Busan D.A., Butter H. Godleu E., Center A., Chandra I.,
RA Burtis K.C., Busan D.A., Butter H., Godleu E., Center A., Chandra I.,
RA Burtis K. Cavily S., Dahlke C., Davenport L.B., Davies P.,
RA Borson D., Bornes M., Dogan Rochs S., Dunkoy B.C., Dunn P.,
RA Bartis M.L., Harvy D., Heinan T.J., Heinander J.R., Houlen P.,
RA Bartis M.L., Harvy D., Heinan T.J., Hell W.H., Glasser K.,
RA Goog F., Gorrell J.H., Ou S., Galbart W.H., Theywan C.,
RA Kimmel B.E., Kodita C.D., Kraft C. Kravitz S., Kulp D., Lal Z.,
RA Hartis M., Kalush F., Karpen G.H., Rez., Kennison J.A., Ketchum K.A.,
RA Hartis M., Kalush F., Karpen G.H., Rez., Kennison J.A., Ketchum K.A.,
RA Hartis M.W., Mutyp D., Mutyp L., Mutyp L., Mutyp J., Moshreti A.,
RA Harkulow G., Milshina N.Y., Wobarry C., Morris J., Moshreti A.,
RA Rakon D.R., Nelson R.A., Milkon K., Nussken D.R., Nelson D.L.,
RA Rakon D.R., Nelson R.A., Milkon K., Nussken D.R., Pecleb M.G.,
RA Rakon D.R., Nelson R.A., Milkon K., Nussken D.R., Pecleb M. M.,
Raholan D.R., Nelson R.A., Milkon K., Nussken D.R., Pecleb M. M.,
Raholan D.R., Nelson R.A., Milkon K., Nussken D.R., Pecleb M.,
Raholan D.R., Pecker M., Wilkon K., Nussken D.R.,
Raholan D.R., Pecker M., Wilkon R., Pecker M.,
Raholan D.R., Pecker M., Wilkon R., Wollen D. M.,
Raholan D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
09V6W7
1D 09V6W7
1D 09V6W7
1D 09V6W7
1D 09V6W7
1D 01-MAY-2000 (TERBLEAL 13, Created).
DT 01-MAY-2000 (TERBLEAL 13, Last sequence update)
DT 01-MAY-2000 (TERBLEAL 16, Last sequence update)
DD MAR RAPTA-2010 (TERBLEAL 16, Last sequence update)
DD MAR RAPTA-2010 (TERBLEAL 16, Last sequence update)
DD MAR RAPTA-2010 (TERBLEAL 16, Last sequence update)
CD ELMENYOTE; Metapood 11, Last sequence update)
CD ELMENYOTE; Metapood 11, Last sequence update)
CO ELMENYOTE; Metapood 11, Last sequence update)
                                                                                                     DD 1198 GOGGOOGHMGPGAANNMOMOCLLOG------GOSGGG------GNAMASOMOMTSMH-WT 1244
22 QOHEDSSQOSPSAGSEQQLDQLLAMPIMMALQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ligon D. K., Netgon K., Naxon, N. Musanett D. F., Puri V., Reese M., Ilazzol M., Pittman G.S., Pan S., Pollard J. V., Reese M., Lincert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Nue B.C., Stden-fidmon J., Simpon M., Skupski M.P., Smith T., Ner E., Spradling A.C., Stapleton M., Strong R., Sun E., Lisakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Mng S. V., Wassarman D.A., Welnstock G.M., Weissenbach J., Norley K.C., Wu D., Yang S., Yao Q.A.,
                                                                                                                                                                                                                                                                                                                 DD 1245 QTQQQITMQQQQQEVQSTTTTHQQQQMMQMGPGGGGGGGGGGGGSANNNNGG 1295
                                                                                                                                                                                                                   82 QMLMQIVMQLMQN-----------QGAGMGGGGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; mam.
; 167263 MW; D4236DA26F70D092 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
MEDLINE-20196006; Pubmed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn00264
SEQUENCE 1594 AA;
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16.5%; Score 96.5; DB 5; Length 1366; 28.8%; Pred, No. 0.073;

Ouery Match Best Local Similarity

09C6M3 RESULT 12 09C6M3 ID 09C6M3 AC 09C6M3

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us-09-829-124-2.rspt

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087264 PRELIMINARY; FKH; ***....087264 987264, 012764 01-NOV-1998 (TrEMBLrel, 08, Last sequence update) 01-UNV-2001 (TrEMBLrel, 08, Last sequence update)
          01-DEC-2001 (TremBLrel. 19, Last annotation update) F47A4.2 PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 3424 SNQMQFQGVRQGQQGMG--GMGGSG 3446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 · LTQMLMQIVMQLMQNQGGAGMGGGG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99069613; Pubmed-9851916;
                                                                                                            Canorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Caer
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theologies A., Excer J.R., Pann C.J., Federspiel N.A., Kaul S., A. Wilte O., Adnoso J. Alfati H., Araulo R., Bowman C.L., Brooks S.Y., An Burkle O., Adnoso J., Alfati H., Araulo R., Bowman C.L., Brooks S.Y., An Bunkle E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Duny M.K., Cross Y.H., Conn L., Conowy A.B., Conway A.R., Cross Y.H., Dewar K., Dunn P., Etgu P., Etdülyum T.V., Peng J.-D., Fong B., Fulli C.Y., Bulli J.E., Goldamith A.D., Haas B., Hansen N.F., Happes B., Huitar I., Han C.J., Con H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Lin R.-Liu S.X., Liu S.X., Liu S.X., Liu Z.A., Lucos J.S., Malti R., Marzialli A., An Hitscher J., Miranda W., Nurson W., Rooney T., Rooley D., As Bahno H., Salterg S.L., Schwattz J.R., Malti R., Marzialli A., Salterg S.L., Schwattz J.R., Shin P., Southvick A.W., Sun B., Tallon L.J., Tambunga G., Torlumi W.J., Town C.D., M. Bull Charlock T., Tambunga G., Torlumi W.J., Town C.D., M. Hu D., Yu G., Fraser C. M., Wonter J.C., Davis R.W.; V. W. G., Fraser C. M., Wonter J.C., Davis R.W.; H. D., Yu G., Fraser C. M., Wonter J.C., Davis R.W.; Selegience and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                     1426 QQQQQQHKGPGAANNQHQQLLQQ------QQSGGG------GNPMASQHQMTSMH-MT 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryots, Viidiplandes (Ereptopphyte Embryophyte; Tracheophyte; Eukaryots, Viidiplandes (Ereptophyte Embryophyte; eudiocts; Rosidae; euramtophyte; Magnoliophyta; eudiocytledons; core eudiocts; Rosidae; euradida II; Erssicales; Erassicaceae; Arabidopsis.
Best Local Similarity 28.8%; Pred. No. 0.086;
Matches 32; Conservative 7; Mismatches 39; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 ОННОООООООООООООНОІТОІДНИН----ООООООАБРІМОМОООТБРІМ 491
                                                                                                            22 QQHEDSSQQSPSAGSEQQLDQLLAMFIMMALQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oubery which 16.4% Score 96; DB 10; Length 534; Best Local Similarity 34.1%; Pred. No. 0.028; Best Local Similarity 41.1%; Pred. No. 0.028; A Hatches 31; Conservative 4; Mismatches 44; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 QOHEDSSQQSPSAGSEQQLDQLLANFIMANLQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                      B2 ONLMOIVMOLMON-------OGGAGMGGGGGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 408:816-820(2000).

**Brait, #0.079281, #0.850810.1; -.

**Brocherical protein:

**SEQUENCE 534 AA, 57273 HW; 7498816724021101 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, Created)
-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 57.3 KOA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 020497 PRELIMINARY, PRT; 3498 AA.
020497, 0204047, 0204040, 01.WOY-1996 (TYEMBLRel. 01. Created)
01-JUN-1998 (TYEMBLRel. 06, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 ONLMOIVMOLM ----- ONQGGAGMGGG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       492 ONDOCODPONYMGGOAFAQAPGRSQQGGGG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDLINE-21016719; PubMed-11130712;
heologis A., Ecker J.R., Palm C.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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RESULT 13 Q20497 ID Q20497 AC Q20497, DT 01-NOV-DT 01-JUN-

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3369 GOOGHO--POOSOISOCOCOCOCOONRINGAACMOCOPTACCOONRIG--MPSC-COSCAAY 3423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The Pseudomonas syringae pv. tomato HrpW protein has domains similar to harpins and pectate lyases and can elicit the plant hypersensitive response and bind to pectate.";
J. Baccertol. 1805:211-5217(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 GPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQQEGLSP 79
oda; Chromadorea; Rhabditida; Rhabditoidea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIRMINE_DOSANON;
MEDITRE_DOSANON;
MIRED_STREE_DOSANON;
MIRED_TR. Charkrowist A.O., Deng W.L., Badel J.L.,
MIRED_STREES_DOSANONS A.D., DENG W.L., BADEN B. A.D., STREET DENG W.L.,
MIRED_STREES_DOSANONS A.D., DENG W.L., BADEN MIRED_STREET DENG W.L.,
MIRED_STREES_DOSANONS A.D., DENG W.L.,
MIRED_STREET, DENG W.L.,
MIRED_S
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Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
NCBL_TaxID-323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 37.64; Pred, No., 0.58; DB 5; Length 3498;
Best Local Similarity 37.64; Pred, No., 0.58;
Makches 32; Conservative 4; Mismatches 42; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-DC3000;
MEDLINE-96422476; Pubmed-9748456;
Charkowski A.O., Alfano J.R., Preston G., Yuan J., He S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for Investigating bloology":
Lace 281:2012-2018(1989).
EMBL: 249888: CAA90064.1; -
InterPro. 1PR0005261; EGF-11Ke.
INTERPO. 1PR000504; RRW.
PROSITE: PS000201; EGE-1; UNKNOWN.1.
PROSITE: PS000201; ENE. INT. UNKNOWN.1.
SEQUENCE: 3498 AA: 400777 MM: 283FFC65A689E336 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          (orthmore B J .; submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
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Ouery Match 15.7%; Score 91.5; DB 2; Length 424; Best Local Similarity 27.8%; Pred. No. 0.068; Matches 27; Conservative 16; Mismatches 27; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 DSSQOSPSAG----SEQOLDQLLAMFIMMIQQSQGSDANQECGNEQPQNCQQEGLSPL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ouery March 15.6%; Score 91; DB 5; Length 624;
Best Local Similarity 28.1%; Pred. No. 0.12;
Matches 27; Conservative 10; Mismarches 37; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 QQHEDSSQQSPSAGSEQQLDQLLAMFINAMLQQSQGSDANQECGNEQPQNGQQ---- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loomis W.F.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U66913, AAB07544.1;
NOW TER 624 624.1; SO343A91ECB0CB37 CRC64;
EMBL; AF005221; AAC62526.1; -.
EMBL; AF232004; AAF71503.1; -.
SEQUENCE 424 AA; 42910 MH; 7AF4ED059BF79D2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           094486 PRELIMINARY, PRT; 624 AA. 049486, 01-FEB-1997 (TrEMBLrel. 02, Created) 01-FEB-1997 (TrEMBLrel. 02, Last sequence update) 01-FEB-1997 (TrEMBLrel. 02, Last annotation update) 01-FEB-1997 (TrEMBLrel. 02, Last annotation update) 01-FEB-1997 (TrEMBLR). 02, Last annotation update) 01-FEB-1997 (TrEMBLR). 03, La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 TOMIMOIVMOLMONOGGAG-----MGGGGSVNSSLGG 112
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Search completed: June 28, 2002, 10:23:23 Job time: 150 sec

OM protein - protein search, using sw model

Run on:

June 28, 2002, 10:19:58; Search time 12.31 Seconds (without alignments)
358.573 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-829-124-2 584 1 MDSIGNNFSNIGNLOTMGIG........OGGAGMGGGGSVNSSLGGNA 114

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 105224 seqs, 38719550 residues Searched:

105224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	tion	erwinia amv	ralstonias	drosophila	saccharomyc	homo sanien	drosophila	drosophila	aedes aegyp	drosophila	saccharomyc	triticum ae	mus musculu	triticum ae	bos taurus	eimeria ten	caenorhabdi	bacillus su	saccharomyc	drosophila	drosophila	drosophila	mus musculu	homo sapien	drosophila	dictyosteli	xenopus lae	homo sapien	homo sapien	saccharomyc	drosophila	drosophila	xiphophorus	homo sapien
	Description	00100	09rbs0	P21519	P33417	009472	001295	P23241	P49880	P20227	P32521	P08488	P54728	P10387	028009	P15714	P34333	P37483	P25367	P20105	P11536	P28285	061471	P35637	P13468	P34099	Q9w705	09u136	P54727	P35732	P33244	P13709	002193	P13645
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SUMMARIES	QI	HRPN_ERWAM	POPA_RALSO	MAM_DROME	IXR1_YEAST	P300_HUMAN	BRC1_DROME	ELAV_DROVI	ECR_AEDAE	TF2D_DROME	PAN1_YEAST	GLT3_WHEAT	R23B_MOUSE	GLTO_WHEAT	FUS_BOVIN	LP61_EIMTE	YKZ6_CAEEL	YYCA_BACSU	YCC8_YEAST	E74A_DROME	E74B_DROME	5HTA_DROME	TOB1_MOUSE	FUS_HUMAN	K10_DROME	KAPC_DICDI	NCO2_XENLA	Z236_HUMAN	R23B_HUMAN	YKF4_YEAST	FTF1_DROME	FSH_DROME	BDNF_XIPMA	K1CJ_HUMAN
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e e	Query	19.0	18.8	16.5	15.3	٠		14.8	14.6	14.2	14.1	13.9	13.5	13.5	13.4	13.4	13.4	13.2	13.1	13.1	13.1	13.0	12.8	12.8	12.8	12.8	12.8	12.8	12.7	12.6	12.6	12.6	12.5	12.5
	Score	111	110	96.5	89.5	88	ന	86.5	82	. 83	82.5			79	78.5	78	7.8	77	76.5	76.5	76.5	7.6	7.5	75	2.4.5	74.5	74.5	٠	74	73.5	73.5		73	73
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	P18480 saccharomyc	P56959 mus muscuju	004047 drosophila	P70605 rattus norv	P02833 drosophila	P34291 caenorhabd1	P32505 saccharomyc	P03210 epstein-bar	P08106 gallus gall	09z1e9 cricetulus	019132 orvetolagus	PO4730 triticum ae		
	SNF5_YEAST	FUS_MOUSE	NONA DROME	KCN3_RAT	HMAN_DROME	YKO3_CAEEL	NAB2_YEAST	YRR2_EBV	HS70 CHICK	GLG1 CRIGR	NOS1_RABIT	GDB3_WHEAT	Constitution 14	ALIGNMENTS
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Ċ	/ 3	72.5	72.5	72.5	72	72	72	72	72	72	72	71.5		
;	34	32	36	37	38	39	40	41	42	43	44	45		

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RESULT HRPN E	RESULT 1
£.	HRPN ERWAM STANDARD; PRT; 403 AA.
S F	(Rel.
T C	39,
DE.	n (Harpin-EA).
N C	HRPN.
38	Elwinia amiyiovola. Bacteria: Proteobacteria: gamma subdivision: Enterchacteriaceae.
8	Erwinia
X A	NCBI_TaxID=552;
R P	(1) SEQUENCE FROM N.A., AND SECIENCE OF 1-15
RC	STRAIN-EA321;
XX Z	MEDLINE=92320301; PubMed=1621099;
RA W	Her E. M., Lany K.J., Zumoli C.H., Bauer D.M., He S.Y., Colimer A., Beer S.V.:
RT	"Harpin, elicitor of the hypersensitive response produced by the
RT	
R R	Science 257:85-88(1992).
RP	REVISIONS.
RC	STRAIN-EA321;
RA	Laby R.J., Kim J.F., Beer S.V.;
<u> </u>	SUMMILLEU (MAK-1999) to the EMBL/GenBank/DDBJ databases.
ខ	: FONCITON: ELECTION HARPIN FILCHES HE IN NON-HOSTS AND IS ALSO
႘	REQUIRED FOR PATHOGENICITY IN HOST PLANTS.
ပ္ပ	-!- SUBCELLULAR LOCATION: SECRETED; VIA THE HRP SECRETION PATHWAY.
3 5	This SWISS-DBOT entry is converient It is and and through a collaboration
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ပ္ပ	the Buropean Bioinformatics Institute. There are no restrictions on its
ე :	use by non-profit institutions as long as its content is in no way
ဗ္ဗ ဗ	modified and this statement is not removed. Usage by and for commercial
ງ ປ	entites equites a license agreement (see http://www.isb-sib.ch/announce/ or send an email to licensedish-sib.ch.
88	or some an email to incensorated air. (ii).
DR	EMBL; M92994; AAC31644.2;
K.	ensitive response.
. L	DOMATH 1 2/0 GLY-RICH.
Š	CE 403 AA; 39697 MW;
Que	Query Match 19.0%; Score 111; DB 1; Length 403;
Mat	best Local Similarity 31.3%; Pred. No. 0.00071; Matches 39; Conservative 21; Mismatches 48; Indels 16; Gaps 7;
Qy	IGNLQTMGI-GPQQHEDSSQQSPS-AGSEQQLDQLLAMFIM
qa	:: :
Qy	57 GSDANQECGNEQPQNGQQEGLSPLTOMLMOIVMOLMONOGGAGMGGGGSVNSSL 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "popA in Ralstonia solanacearum OEI-1 pathogenic to tobacco.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: Act as a specific hypersensitive response (HR) elicitor.
Has activity on tobacco (non-host plant) and petunia but is
without activity on tomato (host plant).
--- SUBCELLULAR LOCATION: Secreted.
--- PTM: POPAZ and popA3 are produced from popA1 by stepwise removal
Arlat M., Van Gijsegem F., Huet J.-C., Pernollet J.-C., Boucher C.A., "Poph, a protein Which induces a hypersensitivity-like response on specific Petunia genotypes, is secreted via the Hrp pathway of Pseudomonas solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the plant pathogen Ralstonia solanacearum.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-GMI1000;
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N
Gasplu C., Lavite M., Moisan A., Robert C., Saurin W., Schlex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hikichi Y., Ikegami M., Okuno T.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                  PopAl protein [Contains: PopA2 protein; PopA3 protein].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypersensitive response; Plasmid; Complete protecome.
                                                                                                                                                                                                                                                                                   Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                          PPPA RALSO STANDARD; PRT; 344 AA. 09RBSO, 052544; 09WXKO; 09RBYO; 01-MAR-2002 (Rel. 41, Created) 01-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hikich Y., Kanda A., Hasegawa H., Okuno T.;
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-94148001; PubMed-8313899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of N-terminal amino acids.
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EMBL; AB026629; BAA77270.1;
EMBL; AB032747; BAA84679.1;
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                                                                                                                                                                                                                                                                                                   Plasmid megaplasmid.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-GMI1000;
                                                111 GGNA 114
                                                                               236 DGSS 239
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                                                                                                                                                                                                                                                                                                                                   Ralstonia
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                                                                                                                                                                                                                                                                                                                                                                                                           118 LLEDLVKLLKAALHMOOPGGNDKGNGVGGANGAKGAGGGGGLAEALQEIEQILAQLGGGG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                     44; Gaps
                                                                                                                                                                                                                                                                                                             3 SIGNNFSNIGNLQTM-----GIGPQQHEDSSQQSPSAGSE------QQLDQ 42
                                                                                                                                                                                                                                                                                                                                                                            43 LLAMFIMMM-----LQQSQGSDANQECG--NEQPQNGQQEGLSPLTQMLMQIVMQLMQN- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: THE PROTEIN HAS MANY AA HOMOPOLYMERIC DOMAINS: 21 POLY-GLN RUNS (FROM 5 TO 16 AA IN LENGTH), 4 POLY-GLY (6 TO 10 AA), 3 POLY-ASN (3 X 5 AA), 1 POLY-ALA (10 AA) AND 1 POLY-THR (5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: TO OTHER NUCLEAR PROTEINS OF DROSOPHILA, TO CERTAIN YEAST AND MAMMALIAN REGULATORY PROTEINS.
                          POPAS PROTEIN.

TNS -> S (IN STRAIN OEL-1)

ANDPSK -> GA (IN STRAIN 8107).

L -> P (IN STRAIN 0EL-1).

G -> A (IN STRAIN 8107).

MISSING (IN STRAIN 8107).

ADGG -> G (IN STRAIN 0EL-1).

N -> I (IN STRAIN 0EL-1).

G -> A (IN STRAIN 0EL-1).

G -> E (IN STRAIN 0EL-1).

A -> E (IN STRAIN 0EL-1).

A -> E (IN STRAIN 0EL-1).

A -> E (IN STRAIN 0EL-1).
                                                                                                                                                                                                                                                    Length 344;
                                                                                                                                                                                                                                                                                  55; Indels
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MEDLINE-91065516; PubMed-1701150;
Smoller D., Friedel C., Schmid A., Bettler D., Lam L.,
Yedvobnick B.;
                                                                                                                                                                                                                                                 18.8%; Score 110; DB 1; 25.8%; Pred. No. 0.00075; iive 16; Mismatches 55,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          --- QGGAGMGGGGSVNSSLGGN 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 AGAGGAGGGVGGAGGADGGSGAGGAGGANGADGGN 212
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                 PROTEIN.
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                                                                                                                                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 40; Conserv
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P21519;
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SEQUENCE FROM N.A.
                   Rieger
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       and for commercial
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              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                             1428 QQQQQQHMGPGAANNMQMQQLLQQ------QOSGGG-----GNMMASQMQMTSMH-MT 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purnelle B., Skala J., van Dyck L., Goffeau A.; "Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new TRNA gene and four new open reading frames including a leucine zipper protein and a homologue to the yeast mitochondrial regulator ABF2."; Yeast 10:125-130(1994).
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                          QQHEDSSQQSPSAGSEQQLDQLLAMFIMMLQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93342489; PubMed-8342024;
Brown S.J., Kellett P.J., Lippard S.J.;
"Ixrl, a yeast protein that binds to platinated DNA and confers
sensitivity to cisplatin.";
Science 261:603-605(1993).
                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                    16.5%; Score 96.5; DB 1; Length 1596; 28.8%; Pred. No. 0.087; Live 7; Mismatches 39; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-UNN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Intrastrand crosslink recognition protein (Structure-specific
                                                                                                                                                                                                                                                                                                                                                                                 QTOQQITMQQQQQFVQSTTTTHQQQQMMQMGPGGGGGGGGGGGGSANNNGG 1525
                                                                                                                                                                                                    ALA-RICH.

8 X 2 AA TANDEM REPEATS OF V-G.

7 X 2 AA TANDEM REPEATS OF G-V.
                                                                                                                                                                                                                                                                                                                                                                    ...----QGGAGMGGGGSVNSSLGG 112
                                                                                                                                                                                              AA TANDEM REPEATS OF G-V.
                                                                                                                                                                                                                                              ASP/GLU-RICH (ACIDIC).
W; B944D86EF359D605 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomycetales; Saccharomycetaceae; Saccharomyces.
      Usage
                                                                                                     ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                       597 AA
modified and this statement is not removed
entities requires a license agreement (See
or Send an email to license@isb-sib.ch).
                                                                                                                                   GLY/ASN-RICH
                                                                                                                                          GLN-RICH.
GLY-RICH.
GLN-RICH.
                                                                                 1; Repeat.
GLN-RICH.
                                                                                                             GLN-RICH.
                                                                                                                                                                                  GLN-RICH.
5 X 2 AA
                                                                                                                                                                           GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IXRI OR ORDI OR YKL032C OR YKL245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94262309; PubMed-8203146;
                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
                                        EMBL; X54251; CAA38152.1; -.
                                                                                                                                                                                                                                                       167717
                                                  PIR; A33106; A33106.
PIR; A36391; A36391.
FlyBase; FBgn0002643; mam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   · (SSRP)
                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                   OMLMOIVMOLMON----
                                                                                Neurogenesis; Nuclear
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                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288C
                                                                                                                                                                                                                                                                                                      32;
                                                                                                                                                                                                                                                                                                                                                                                                                                     IXR1_YEAST
P33417:
                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                             DOMAIN
SEQUENCE
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                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                  82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSDANQECG----NEQPQNGQQEGLSP----LTQMLMQIVMQLMQNQGGAGMGGGGSV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 QQQQQQQQQQQQQQQQQQQQQQVYYPLPPQSLTQPTSQSQQQQQQQQQQQQQANSNSNS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSIGNNFSNIG----NLQTMGI---GPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQ 56
                                    MEDLINE-94316692; PubMed-8041793; MEDLINE-94316692; PubMed-8041793; Lambert J.R., Bilanchone V.W., Cumsky M.G.; Lambert J.R., Bilanchone V.W., Cumsky M.G.; The ORDI gene encodes a transcription factor involved in oxygen regulation and is identical to IXRI, a gene that confers cisplatin sensitivity to Saccharomyces cerevisalee.; Proc. Natl. Acad. Sci. U.S.A. 91:7345-7349(1994).

-I- FUNCTION: BINDS TO PLATINATED DNA AND CONFERS SENSITIVITY TO THE ANTICANCER DRUG CISPLATIN. ACTIVATE THE EXPRESSION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00398; HMG; 2.
DNA-binding; Nuclear protein; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF3B705AA2C5AC74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN REF. 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 89.5; DB
; Pred. No. 0.15;
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y -> F (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A -> T (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOX 1.
                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLN-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000910; HMG_12_box. Pfam; PF00505; HMG_box; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67856 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X71622; CAB37853.1; -. EMBL; Z28032; CAA81867.1; -. EMBL; L16500; AAA02859.1; -. HSSP; P07155; 1AAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.3%;
28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00398; HMG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
93
114
207
220
220
597 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S0001515; IXR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSFAC; T01849;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 NSSLGGNA 114
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281
565
                                                                                                                                                                                                                                             COX5B GENE.
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ID P300_HUMAN
AC Q09472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA_BIND
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us-09-829-124-2.rsp

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STRAIN-BERKELEY;
                                                                                                                           2249 LGAEA 2253
                                                                         110 LGGNA 114
                                                                                                                                                                                                                                                   BRC1_DROME
                                                                                                                                                                                                  RESULT · 6
BRC1_DROME
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                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Ewropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                            MEDLINE-95011587; PubMed=7523245; Eckner R., Ewen M. E., Newsome D., Gerdes M., Decaprio J.A., Eckner R., Ewen M. E., Newsome D., Gerdes M., Decaprio J.A., Lavingston D. M.;

Molecular cloning and functional analysis of the adenovirus ElA-associated 300-kp protein (p300) reveals a protein with properties of atranscriptional adaptor...

Genes Dev. 8:869-884(1994).

-!- FUNCTION: PROBABLE TRANSCRIPTIONAL ADAPTOR REQUIRED FOR THE ACTIVITY OF CERTAIN COMPLEX TRANSCRIPTIONAL REQUIRED FOR THE ACTIVITY OF CERTAIN COMPLEX TRANSCRIPTION. BINDS TO AND MAY BE INVOLVED IN THE TRANSFORMING CAPACITY OF THE ADENOVIRUS ELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2132 NMNPMQAGVQRAGLPQQQPQQQLQPPMGGMSPQAQQMNMNHNTMPSQFRDILRRQQMMQQ 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 NLQTMGIG-----PQQHEDSSQQSPSAGSEQQLDQ------LLAMFIMMML 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50135; ZF_ZZ_2; 1.
Transcription regulation; Nuclear protein; Bromodomain; Cell cycle;
Zinc-finger.
                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING REGION FOR ELA ADENOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 88; DB 1; Length 2414;
Pred. No. 0.96;
5; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
POLY-GLU.
POLY-GLN.
POLY-GLN.
W. GBFF909EE4B9D693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: CONTAINS 1 BROMODOMAIN.
-!- SIMILARITY: CONTAINS 1 ZZ-TYPE ZINC FINGER.
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PRODSO3; BROMODOMAIN.
SMART; SMO1297; BROMO; 1
BRART; SMO1291; ZNF_ZZ,
PROSITE; PSO633; BROMODOMAIN_1;
PROSITE; PSSO014; BROMODOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001487; Bromodomain. IPR003101; KIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000197; TAZ_finger.
InterPro; IPR000433; ZnF_ZZ.
Pfam; PF00439; bromodomain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
9
                                                                                         Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U01877; AAA18639.1; -.
TRANSFAC; T01427; -.
MIM; 602700; -.
                    ElA-associated protein p300.
EP300 OR P300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.1%;
31.2%;
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Pfam; PF02135; zf-TAZ; 2.
Pfam; PF00569; ZZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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1139
1818
1707
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2069
2195
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                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                            SEQUENCE FROM N.A.
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Matches 39; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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ZN_FING
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53 QOSQGSDANQECG---NEQPQNGQQEGLSPLTQMLMQIVMQLMQNQGGAGMGGGGSVNSS 109

\$ 6 6 ô

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110 LIGGNA 114

DD 2349 [CAREA 225]

RESEULT. 6

BRESULT. 7

BRESU
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AE003421; AAF45648.1; AE003421; AAF45651.1; ALT_SE0. AL009146; CAA15629.1; ALT_SE0. AL009146; CAA15628.1; AE009146; CAA15628.1;

EMBL; X54666; CAA38477.1; -. EMBL; X54665; CAA38476.1; -. EMBL; X54663; CAA38474.1; -. EMBL; X54664; CAA38475.1; -.

EMBL;

EMBL; EMBL; EMBL; TRANSFAC; T01479; -. F1yBase; F8pr0000210; br. InterPro; IPR000210; BTB_PO2. InterPro; IPR000822; Znf-C2H2.

FRANSFAC;

SMART; SM00225; BTB; 1. SMART; SM00355; ZnF_C2H2; 2.

Pfam; PF00651; BTB; 1. Pfam; PF00096; zf-C2H2; 2.

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Bayer C.A., Holley B., Fristrom J.W.;
"A switch in broad-complex zinc-finger isoform expression is regulated posttranscriptionally during the metamorphosis of Drosophila imaginal
                                                                                                                                                                                                                                                                                                                                       [5]
DEVELOPMENTAL STAGE.
MEDLINE-94038699; PubMed-8223281;
Huet F., Ruiz C., Futards G.;
Fuffs and PCR: the in vivo dynamics of early gene expression during ecdysone responses in Drosophila.";
Development 118:613-627(1993).
                                                 Benos P.V. Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
Dreano S., Gloux S., Lelaure V., Mottler S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden Kiamos I., Bolshakov S.,
Modolel J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Scheefer U., Jaeckle H., Bucheton A.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
                                                                                                                                          Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
MCMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.
                                                                                                                                                                                   "From sequence to chromosome: the tip of the X chromosome of D.
             EQUENCE FROM N.A. (ISOFORMS TNT1-Q1-Z1; Z2 AND NS-Z3).
                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE, AND CHARACTERIZATION OF ISOFORMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION OF ISOFORMS, AND MUTATIONAL ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-97384928; PubMed-9242423;
Bayer C.A., von Kalm L., Fristrom J.W.;
                                      MEDLINE-20196011; PubMed-10731137;
                                                                                                                                                                                                                                               TISSUE-Larva, and Imaginal disks;
MEDLINE-96299417; PubMed-8660872;
                                                                                                                                                                                                        Science 287:2220-2222(2000).
                                                                                                                                                                                                                                                                                                                             Dev. Biol. 177:1-14(1996)
                                                                                                                                                                                               melanogaster.
                                                                                                                                                                      Glover D.M.;
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PROSITE; PS50097; BTB; 1.
PROSITE; PS50097; BTB; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
Nuclear protein; DNA-binding; Developmental protein; Zinc-finger; Metal-binding; Alternative splicing.

LOW LEVELS IN WING DISK.
INDUCTION: PRIMARY RESPONSE TO 20-HYDROXYECDYSONE IN THIRD INSTAR

SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.

LARVAL IMAGINAL DISKS.

NSLRNHKSIYHRNLKQPKQEPGVGATQAAANSFYHQQHQQQ QLNHHSSS -> PHSITRSAATSPTSSTSSPPSPPTALISP TSSLKGSLAAAVYSLHSHAHGHVLGHATSPPRPGSVGSSVG SNLCTSTSMGCGVNSGNNSGNNGNNANNNSNNGNATNNN 51; Indels 20; Gaps 5 GNNFSNIGNLØTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQEC 64 Length 727; DB 1; 10; Mismatches Score 87; Pred. No. (14.9%; 28.3%; Conservative Best Local Similarity Matches 32; Conserv Query Match ò g

KLTTNATTTTTINNSITNNNNNNNNNYDYSLPTKNSNSO KTPSPTTTTLTTPTTTTPTRPTAITSASGICGLNLSTFAAN
-> NSPKKLFSCQLCGKLLCSKASLKRHIADKHAVRQEEYR

MISSING (IN ISOFORM BRCORE-01-21)

ZINC-FINGERS

ZN_FING VARSPLIC

ZN_FING

/ARSPLIC VARSPLIC

POLY-ALA. POLY-GLN.

POLY-GLN

DOMAIN OMAIN OMAIN

POLY-THR. POLY-ASN.

DOMAIN DOMAIN OMAIN

DOMAIN OMAIN

SSI (IN ISOFORM BRCORE-22).
MISSING (IN ISOFORM BRCORE-22).
KLTINATTTTTINNSITNNNNNNNNNNYDYSLPTKNSNSQ CAICERVYCSRNSLMTHIYTYHKSRPGEMEMKDIKLYNQFN

727

VARSPLIC VARSPLIC

KTPSPTTTLTTTTTTTTTTTAITSASGICGLNLSTFAAN GSSSGGSNGGLSMTALLPQQQQQQQQQQHQMSQQQQQQQQQ QQQGNSSSGQQQPNGILACSTPKANTPTTTQQQMYAAVMA **AAASASASTSGSANSSLNNSNSTLNTSGGLNNSASGGDDFR** CNPCNKNLSSLTRLKRHIQNVHMRPTKEPVCNICKRVYSSL

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                                                                                                                                                                                                                        Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                        MEDLINE-91246165; PubMed-1903840; Yao K.-M., White K.; Organizational analysis of elav gene and functional analysis of ELAV protein of Drosophila melanogaster and Drosophila virilis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 LQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQ 73
                                                                                                                                                                                                                                                                                                                                                                                                      65 GNEQPQNGQQEGLSPL----TQMLMQIVMQLMQNQGGAGMGGGGSVNSSLGGN 113
                               564 GOOOOPNGILACSTPKANTPTTTQQQMYAAVMAAAASASASTSGSANSSLNNS 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.8%; Score 86.5; DB 1; Length.519; 27.8%; Pred. No. 0.25; tive 14; Mismatches 49; Indels
                                                                                                                                          01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Elav protein (Embryonic lethal abnormal visual protein).
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RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 QEGLSPLTQMLMQIVMQLMQ--NQGGAGMGGGGSVNS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147 QQQQQVVQQQVQQQANTNGNSGGAQNGSNGSTET 183
                                                                                                                 519 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002343; Hud_Sxl_RNA.
InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A40252; A40252.
HSSP; P19339; 2SXL.
FlyBase; FBgn0013110; Dvir\elav
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PROSITE; PS00030; RRM_RNP_1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00076; rrm; 3.
PRINTS; PR00961; HUDSXLRNA.
SMART; SM00360; RRM; 3.
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Best Local Similarity
Matches 27; Conserva
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=7244;
                                                                                                              ELAV_DROVI
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                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY. NRI SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ecdysone receptor (Ecdysteroid receptor) (20-hydroxy-ecdysone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
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NUCLEAR RECEPTOR-TYPE.
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InterPro; IPR001723; Strdhormone_receptor.
InterPro; IPR001628; zf-C4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
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S; Pred. No. 0.47
10; Mismatches
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                                                                                                                                                                                                                                                       Aedes aegypti (Yellowfever mosquito).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fat body;
MEDLINE=95227190; Pubmed=7711747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
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29.68;
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                                                                                                                                                                            receptor) (20E receptor).
ECR OR NR1H1.
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190
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Best Local Similarity
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ZN_FING
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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkov C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bulck H., Cadleu E., Center P.,
RA Buttis K.C., Busam D.A., Butler H., Cadleu E., Center P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays-A.D., Dew I., Dietz S.M.,
RA Buttis K.C., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Bodson K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosher C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Guz., Gunn P., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wein M. H., Ibegwam C.,
Jalali M., Kalush F., Katpen G.H., Ka Z., Kennison J.A., Ketchum R.A.
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                         P20227; OBWING.
P20227; OBWING.
D1-FEB-1991 (Rel. 17, Created)
O1-FEB-1991 (Rel. 17, Last sequence update)
O1-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transcription initiation factor TFIID (TATA-box factor) (TATA sequence-binding protein) (TEP) (TATA-box binding protein).
TEP OR FPIID ON BFFI OR CG984.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diosophilae; Drosophilae.
                                     22 QQHEDSSQQSPSAGSEQQLDQLLAMFIMMILQQSQG-SDANQECGNEQPQNGQQ----E 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-90304877; PubMed-2194666;
Hoey T., Dynlacht B.D., Peterson M.G., Pugh B.F., Tjian R.;
"Isolation and characterization of the Drosophila gene encoding the
TATA box binding protein, TFIID.";
Cell 61:1179-1186(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muhich M., Iida C.T., Horikoshi M., Roeder R.G., Parker C.S., "cDNA clone encoding Drosophila transcription factor TFIID.", Proc. Natl. Acad. Sci. U.S.A. 87:9148-9152(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee R., Oh Y., Yoon J., Cho N., Baek K.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lira-Devito L.M., Burke T.W., Kadonaga J.T.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases
                                                                               627 QLTPNQQQHQQHSQLQQVHANGSGGGGSNNNSSSGG 664
                                                                                                                                                                                                                                    353 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91067664; PubMed=2123550;
                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                    RESULT 9
TF2D_DROME
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

Radonb S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Radonb S.M., Nelson K.A., Nixon K., Nisskern D.R., Pacleb J.M.,

Radazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Radon S.R., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Radon B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Radon B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Radon S.V., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,

Williams S.M., Myers E.W., Rubin G.M., Venter J.C.,

Radon S.M., Myers E.W., Rubin G.M., Venter J.C.,

"The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195(2000)

C. - FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION

OF EUKARYOTIC GENES TRANSCRIEBED BY RNA POLYMERASE II. TFIID BINDS

SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO
                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 PLAHKOMOSYOPSASYQQQQQQ-----QQLQSQAPGG-----GGSTPQSMMQ----PQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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POLY-GLN.
POLY-GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83; DB 1; Length 353;
Pred. No. 0.36; . .
9; Mismatches 38; Indels
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7B079BC01BAF69BC CRC64;
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                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Nuclear.
-1- SIMILARITY: BELONGS TO THE TBP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 TQMLMQIVMQLMQNQ--GGAGMGGGGSVNSSL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TPOSMMAHMMPMSERSVGGSGGGGDALSNI 153
                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: BINDS DNA AS A MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0686; TIFACTORIID. PROSITE; PS00351; TFIID; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38451 MW;
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Pfam; PF00352; TBP; 2.
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PIR, A38416, A38416.
HSSP, P20226, 1CDW.
TRANSFAC, T00797; -.
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353 AA;
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P32521;
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CONFLICT
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PAN1_YEAST
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01-OCT-1993 (Rel. 27, Created)

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Query Match 14.1%;
Best Local Similarity 27.6%;
Matches 29; Conservative
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575
680
350
680
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1101
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34
106
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P08488;
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GLT3_WHEAT
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                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: NOT KNOWN.
-!- PTW: THE N-TERMINUS IS BLOCKED.
-!- SIMILARITY: SOME TO MAMMALLIAN EPS15.
-!- CAUTION: WAS ORIGINALLY THOUGHT TO BE A SUBUNIT OF PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE.
                                                                                                                                                                                                                                                                            Voss H., Tamames J., Teodoru C., Valencia A., Sensen C., Wiemann S., Schwager C., Zimmermann J., Sander C., Ansorge W.; "Nucleotide sequence and analysis of the centromeric region of yeast chromosome IX.";
                                                                                                                                                         STRAIN-S286C / AB972;
Barrell B.G. Badcock K., Bankier A.T., Bowman S., Brown D., Churcher C.M., Connor R., Copsey T., Dear-S., Devilin K., Fraser A., Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Whitehead S., Walsh S.V., Whitehead S., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 320-344; 352-375 AND 899-906. MEDLINE-92405166; PubMed=1339314; Sachs A.B., Deardorff J.A.; "Translation initiation requires the PAB-dependent poly(A) ribonuclease in yeast.";
                                                 Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA APPROXIMATE REPEATS.
                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
01-FEB-1995 (Rel. 31, Last sequence update)
01-NoV-1997 (Rel. 35, Last annotation update)
                           OR MIP3 OR MDP3 OR YIR006C OR YIB6C.
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IF; S48440; S48440.
SGD; S0001445; PAN1.
InterPro, IPR000261; EPS15_repeat.
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403
420
433
509
518
549
                                                                                                                                 Cell 70:961-973(1992)
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                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                   SEQUENCE FROM N.A
                                                                  NCBI_TaxID-4932;
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A -> R (IN REF. 1).
GGVLPPPPPLPTQQASTSEPIJAHVDNYNGAEKGTGAYGS
DSDDDVLSIPESVGTDEEEEGAQPVSTAGIPSIPPAGIPP
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KKARAHMDPILMMTFYRFLNQLVQMKRKKGHNQFLLQVSH
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STRAIN-CV. CHINESE SPRING;
MEDLINE-86041882; Pubmed-3840588;
Thompson R.D., Bartels D., Harberd N.P.;
"Nucleotide sequence of a gene from chromosome 1D of wheat encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 QQQGMGYQQQQQQQQQQQQPNG-----FYPQQQQGQSSNQPQGQPQQMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P -> T (IN REF. 1).
TAGDODAR -> YYCKSGKN (IN REF. 1).
MISSING (IN REF. 1).
MISSING (IN REF. 1).
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W; F3518495FF759553 CRC64;
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Pred. No. 2;
9; Mismatches 44; Indels 23
2 x 23 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                                                    AA APPROXIMATE REPEATS
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01-AUG-1988 (Rel. 08, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Glutenin, high molecular weight subunit 12 precursor.
                                                                           AA TANDEM REPEATS
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POLY-PRO.
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POLY-GLN.
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8 x
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4

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416 AA;
                                          58 kDa SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4565;
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Best Local Simi
Matches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLTO_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                  -i-MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE GROUP 1 CHROMOSOMES OF WHEAT.
-i-MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GQOPGQ AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 GOWQQSGQGGHYPTSLQQPGQGQ-----GHYLASQQQPAQGQGHYPASQQQPGQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                van der Spek P.J., Visser C.E., Hanaoka F., Smit B.,
Hagemeijer A., Bootsma D., Hoeijmakers J.H.J.;
"Cloning, comparative mapping, and RNA expression of the mouse
homologues of the Saccharomyces cerevisiae nucleotide excision repair
gene RAD23.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 31:20-27(1996).
-!- FUNCTION: INVOLVED IN DNA EXCISION REPAIR. MAY PLAY A PART IN DNA
                                                                                                                                                                                                                                                                                                                                            GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 GNLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQN 71
                             STORAGE
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
UV excision repair protein RAD23 homolog B (MHR23B) (XP-C repair
complementing complex 58 kDa protein) (P58).
                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                              13.9%; Score 81; DB 1; Length 660; 27.4%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 GOOEGLSPLTQMLMQIVMQLMQNQGG-----AGMGGGGSVNSS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 GQQ-GHYPASQ-----QQPGQGQQGHYPASQQEPGQQQQQIPAS 355
                                                                                                                                                                                                                                                                                                                  Seed storage protein; Repeat; Multigene family; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                            2BFD09D8C8FCCCFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Mismatches
                                                                                                                                                                                                                                                                 InterPro: IPR001768; Cereal_tryp_amyl_inh.
InterPro: IPR001419; Glutenin.
Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR00210; GLUTENIN.
                                                                                                                                                                                                                                                                                                                                                                   REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BALB/C; TISSUE=Testis; MEDLINE=96403997; PubMed=8808275;
                                                                                                                                                                                                                                                                                                                                                                              70868 MW;
                                                                                                                                                                                                                                EMBL; X03041; CAA26847.1; -. PIR; A24266; A24266.
HSSP; P01088; 1BFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                 GOOPGOGGOGYYPTS.
                                                                                                                                                                                                                                                                                                                                                                125 (
660 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAD23B OR MHŘ23B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R23B_MOUSE
P54728;
                                                                                                                                                                                                                                                                                                                                                                                                                                    29:
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R23B_MOUSE
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'n,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 QQMRQIIQQNPSL----LPALL-------QIGRENPQLLQQ--ISQHQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malpica-Romero J.M.; "Nucleotide sequences of the two high-molecular-weight glutenin genes from the D-genome of a hexaploid bread wheat, Triticum aestivum L. cv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 QQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNGQQEGLSPLT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 17:461-462(1989).
-1- FUNCTION: GLUTENINS ARE THE HIGH MOLECULAR WEIGHT SEED STORAGE PROTEIN OF WHEAT ENDOSPERM. THOUGHT TO BE RESPONSIBLE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (Wheat).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
CHROMATIN STRUCTURE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson O.D., Greene F.C., Yip R.E., Halford N.G., Shewry P.R.,
                         ALLOW ACCESS BY DAMAGE-PROCESSING ENZYMES.
SUBUNIT: HETERODIMER OF A 125 KDa SUBUNIT (P125) AND OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Glutenin, high molecular weight subunit DY10 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13E0245A6D892205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                        58 kDa SUBUNIT (P58).
-1- SUBCELLGLAR LOCATION: Nuclear (Probable).
-1- SIMILARITY: CONTAINS 1 UBLQUITIN-LIKE DOMAIN.
-1- SIMILARITY: CONTAINS 2 UBA DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 79; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UBIQUITIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               648 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 1.1;
9; Mismatches
RECOGNITION AND/OR IN ALTERING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QMLMQIVMQLMQNQGGAGMGGGGGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA damage; DNA repair; Nuclear protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-ALA.
POLY-THR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50053; UBIQUITIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. CHEYENNE;
MEDLINE-89098419; Pubmed-2563152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:105128; Rad23b.
InterPro; IPR0000449; UBA.
InterPro; IPR0000526; Ubiquitin.
Pfam; PF00627; UBA; 2.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43516 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X92411; CAA63146.1; -. HSSP; P54725; 1DV0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.5%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00165; UBA; 2.
SMART; SM00213; UBQ; 1.
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metal-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LP61_EIMTE
P15714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eimeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseé[sb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                       3;
VISCO-ELASTIC PROPERTY OF WHEAT DOUGH.
-!- SUBUNIT: DISULFIDE-BRIDGE LINKED AGGREGATES. ...
-!- MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                               268 SLOOPGOGOGHYLASQOOPGOGOO-----GHYPASQOOPGOGOOGHYPASQOOPGOG 320
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           13 NLQTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMMLQQSQGSDANQECGNEQPQNG 72
                                                                                                                                                                                                                                                                                                      GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alliegro M.C.;
"A C-terminal carbohydrate-binding domain in the endothelial cell
regulatory protein, pigpen: new function for an EWS family member.";
Exp. Cell Res. 255:270-277(2000).
                                GROUP I CHROMOSOMES OF WHEAT.
MISCELLANEOUS: THE MATURE PROTEIN IS CHARACTERIZED BY A LARGE NUMBER OF WELL PRESERVED REPEATS OF THE TWO MOTIFS: GOOPGO AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A nuclear protein regulated during the transition from active to quiescent phenotype in cultured endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                      46; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                    13.5%; Score 79; DB 1; Length 648; 29.8%; Pred. No. 1.8.
                                                                                                                                                                                                                                                                             Seed storage protein; Repeat; Multigene family; Signal
                                                                                                                                                                                                                                                                                                                              REPEATS.
FE98F1D44B9E9AF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 QOEGLSPLTOML ---- MQIVMQLMQNQGGAGMGG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 00-GHYPASQQEPGGGQGGIPASQQQPGQGQQG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 35, Last sequence update) (Rel. 41, Last annotation update
                                                                                                                                                                                                             HSSP, P01088; 1BFA.
InterPro; IPR001768; Cereal_tryp_amyl_inh.
InterPro; IPR001419; Glutenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alliegro M.C., Alliegro M.A.; *A nuclear protein regulated during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                     Pfam; PF00234; tryp_alpha_amyl; 1.
PRINTS; PR00210; GLUTENIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE~20160719; PubMed-10694442; Alliegro M.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Aorta;
MEDLINE-96175600; PubMed-8631501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                         69629 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dev. Biol. 174:288-297(1996).
                                                                                                                                                                                            EMBL; X12929; CAA31396.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYDRATE BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 29.8°
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovinae; Bos.
                                                                                                                                                                                                         S04832; S04832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              taurus (Bovine).
                                                                       GOOPGOGGGYPTS
                                                                                                                                                                                                                                                                                                                                        648 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUS_BOVIN
Q28009;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae;
                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
FUS_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
FUNCTION: BINDS BOTH SINGLE-STRANDED AND DOUBLE-STRANDED DNA AND PROMOTES ATP-INDEPENDENT ANNEALING OF COMPLEMENTARY SINGLE-STRANDED DNAS. AND D-LOOP FORMATION IN SUPERHELICAL DOUBLE-STRANDED DNA. MAY PLAY A ROLE IN MAINTENANCE OF GENOMIC INTEGRITY (BY
                                                                                                                                                                                                                                                         THROUGHOUT (EXCLUDING NUCLEOLI), TOGETHER WITH A SMALL NUMBER OF INTENSELY STAINED FOCAL POINTS, OR GRANULES, AND PUNCTATE STAINING ALONG THE NUCLEAR ENVELOPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSS0102; RRM; 1.
PROSITE; PS00030; RRM; RNP_1; FALSE_NEG.
PROSITE; PS010369; 2F_RANBP2_1; 1.
PROSITE; PS50199; ZF_RANBP2_2; 1.
RNA-binding; DNA-binding; Nuclear protein; Repeat; Zinc-finger; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 QSSGYGQPQGGGYGQQSGYGGQQQSYGQQQSYNPPQGYGQQSQYNSSGGGGGGGGGSYGQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 QTMGIGPQQHEDSSQQSPSAGSEQQLDQLLAMFIMMML-QQSQ-----GSDANQECGN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimerlidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 EQPQ------NGQQEGLSPLTQMLMQIVMQLMQNQGGAGMGGGGGSVNSSLGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
                                                                                                                                                                                                                                 EXHIBITS DIFFUSE STAINING
                                                                                                                                                                      SUBUNIT: COMPONENT OF NUCLEAR RIBOPROTEIN COMPLEXES (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR, EXHIBITS DIFFUSE STAININ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 512;
                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS I RNA RECOGNITION MOTIF (RRM).
SIMILARITY: CONTAINS I RANBP2-TYPE ZINC FINGER.
SIMILARITY: BELONGS TO THE TET FAMILY OF RNP PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 1.5;
6; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3652329C044F1386 CRC64;
                                                                                                                                                                                                                                                                                                                                                   DOMAIN: THE C-TERMINAL DOMAIN BINDS CARBOHYDRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLN/GLY/SER/TYR-RICH. GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 78.5; DB 1;
Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA-BINDING (RRM).
ARG/GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANBP2-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000504; RRM.
InterPro; IPR001876; Znf-RanBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52240 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U26024; AAC13543.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.4%;
29.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00360; RRM; 1.
SMART; SM00547; ZNF_RBZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00076; rrm; 1.
Pfam; PF00641; zf-RanBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen LPMC-61 (Fragment).
Eimeria tenella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
408
412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P09651; 1HA1
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                 SUBUNIT: MAY BE CONALENTLY LINKED BY DISULFIDE BONDS TO OTHER POLYPEPTIDES TO FORM THE 80 kDa ANTIGEN.
DEVELOPMENTAL STAGE: PRESENT IN ALL STAGES THROUGHOUT THE SPORULATION.
EXCYSTATION.
                                                                                                                                                                                                                                                                                          12 X APPROXIMATE TANDEM REPEATS, GLN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8C5E6005FFFC2DB3 CRC64;
                                                                                                                                                                                                                                                                      Antigen; Sporozoite; Repeat; Sporulation.
           MEDLINE-90348718; PubMed-2200963;
                                                                                                                                                                                                                                                                                                                                                                                                                                            255
31267 MW;
                                                                                                                                                                                                                                                 EMBL; M30933; AAA29079.1; -.
                                                                                                                                                                                                                                                                                          210
                                                                                                                                                                                                                                                                                                                                                                                                                                          255
255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                   EPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                      EPEAT
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Query Match 13.4%; Score 78; DB 1; Length 255;
Best Local Similarity 32.6%; Pred. No. 0.79;
Matches 30; Conservative 6; Mismatches 48; Indels 8; Gaps
Oy 22 QQHEDSSQQSPSAGSEQQLDQLLAWFIMMALOOSGGSDANDECGNEDDONGOOFGIGET 81

5;

0 Oy 0 DP

82 QMLMQIVMQLMQNQGGAGMGGGGSVNSSLGGN 113

198 00P00--0000000000CepcvGIVVPYLGSS 227

Search completed: June 28, 2002, 10:22:46 Job time: 168 sec